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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:55:03 ; Search time 24.7145 Seconds

(without alignments)
782.004 Million cell updates/sec

Title: US-09-684-883-2

Perfect score: 868
Sequence: 1 MKKALATLALPAALAE.....VNTVKNRSGELSGVRRKF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	174	AAW04891	Proteinase K resis
2	854	98.4	174	AAW04893	Proteinase K resis
3	825	95.0	174	AAW04894	Proteinase K resis
4	824.5	95.0	175	AAW04892	Proteinase K resis
5	785	90.4	155	AA19895	Neisseria meningit
6	135	15.6	170	AA19311	Neisseria meningit
7	133	15.3	25	AAW04912	N. meningitidis 60
8	94.5	10.9	212	AAU34556	E. coli cellular p
9	94	10.8	353	AA847447	MOMP p5. Haemophil
10	89.5	10.3	257	AAU38252	Salmonella typhi c
11	88.5	10.2	180	AA184612	The outer membrane

12	88.5	10.2	204	20	AA134533	Porphyromonas ging
13	88.5	10.2	221	20	AA134400	Porphyromonas ging
14	88.5	10.2	573	19	AAW68202	M. catarrhalis str
15	88	10.1	610	19	AAW68206	M. catarrhalis str
16	88	10.1	624	19	AAW68204	M. catarrhalis str
17	88	10.1	889	19	AAW68208	M. catarrhalis str
18	87.5	10.1	708	19	AAW73022	Helicobacter pylori
19	87.5	10.1	708	21	AAV78360	N. meningitidis 60
20	87	10.0	16	22	AAW04901	Cysteine protease
21	87	10.0	500	22	AAW65766	Non-typable Haemop
22	86	9.9	359	16	AAW66294	Arabidopsis thalia
23	85.5	9.9	339	21	AAW52873	Arabidopsis thalia
24	85.5	9.9	534	21	AAW09860	Arabidopsis thalia
25	85	9.8	568	17	AAW96210	ATI. protein-malts
26	84	9.7	350	9	AAW82053	Outer membrane pro
27	84	9.7	350	22	AAW59179	Virulence gene pro
28	84	9.6	364	21	AAW44588	Actinobacillus ple
29	83	9.6	364	21	AAW96097	H. pylori outer me
30	83	9.6	364	21	AAW97899	Chlamydia trachoma
31	82.5	9.5	704	20	AAV17210	Arabidopsis thalia
32	82.5	9.5	797	20	AAV36955	M. catarrhalis str
33	82	9.4	433	19	AAW41732	N. meningitidis 60
34	82	9.4	512	20	AAV43382	C glutamincum prote
35	81	9.3	15	17	AAW04909	Attachment-invasio
36	81	9.3	261	22	AAW92581	Arabidopsis thalia
37	80.5	9.3	162	21	AAW96207	Haemophilus influe
38	80	9.2	316	21	AAW52874	Arabidopsis thalia
39	80	9.2	390	18	AAW21678	Blood group antige
40	80	9.2	511	21	AAW09861	Actinobacillus ple
41	80	9.2	511	21	AAW32501	Fibronectin attach
42	80	9.2	707	19	AAW41523	
43	79.5	9.2	215	21	AAV96096	
44	79.5	9.2	215	21	AAV97897	
45	79.5	9.2	325	21	AAV97281	

ALIGNMENTS

RESULT 1	AAW04891	standard; Protein; 174 AA.
ID	AAW04891	
XX	AAW04891	
AC	AAW04891	
XX	AAW04891	
DT	22-DEC-1996	(first entry)
XX	22-DEC-1996	
DE	Proteinase K resistant N. meningitidis 22 kd surface protein.	
XX	Proteinase K resistant; Neisseria meningitidis;	
KW	Neisseria gonorrhoeae; antibody; detection; probe; surface protein.	
XX	Neisseria meningitidis strain 608B.	
OS	Neisseria meningitidis strain 608B.	
XX	Neisseria meningitidis strain 608B.	
FH	Key	Location/Qualifiers
FT	Peptide	1..19
FT	Protein	/label= sig-peptide
FT		20..174
FT		/label= mat_protein
PN	W09629412-A1.	
XX	W09629412-A1.	
PD	26-SEP-1996.	
PF	15-MAR-1996.	96WO-CA00157.
XX	15-MAR-1996.	
PR	04-AUG-1995.	95US-0001983.
XX	04-AUG-1995.	
PR	17-MAR-1995.	95US-0406362.
XX	17-MAR-1995.	
PA	(IAFB-) IAF BIO VAC INC.	
PI	Brodeur BR, Hamel J, Martin D, Rioux C;	
XX	Brodeur BR, Hamel J, Martin D, Rioux C;	

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39039.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 1; 117pp; English.
 XX
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kd antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 XX
 SQ Sequence 174 AA:
 Query Match 100.0%; Score 868; DB 17; Length 174;
 Best Local Similarity 100.0%; Pred. No. 4,1e-87;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKALATLIALALPAALAEAGAGFYVOADAHAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAALAEAGAGFYVOADAHAHAKASSLSGAKGSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKKNYKAPSTDFEKLKYSIGASAIYDFDTQSPVKPYLGARLSINRASVDLGSDSF 120
 DB 61 FAVDYTRYKKNYKAPSTDFEKLKYSIGASAIYDFDTQSPVKPYLGARLSINRASVDLGSDSF 120
 QY 121 SQTSGIGLVLTGVSAYAVTPNVDLDAGRYNYIGKVNTRYKNVRSSELSVGVRKF 174
 DB 121 SQTSGIGLVLTGVSAYAVTPNVDLDAGRYNYIGKVNTRYKNVRSSELSVGVRKF 174
 RESULT 2
 AAM04893
 ID AAM04893 standard; Protein; 174 AA.
 AC AAM04893;
 XX
 DT 22-DEC-1996 (first entry)
 XX
 DE Proteinase K resistant N. meningitidis 22 kd surface protein.
 XX
 KW Proteinase K resistant; Neisseria meningitidis;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
 XX
 OS Neisseria meningitidis strain 24063.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..174
 FT /label= mat_protein
 PN W09629412-A1.
 PD 26-SEP-1996.
 XX
 PF 15-MAR-1996; 96WO-CA00157.
 XX
 PR 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 XX
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39041.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 9; 117pp; English.
 XX
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kd antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 XX
 SQ Sequence 174 AA:
 Query Match 98.4%; Score 854; DB 17; Length 174;
 Best Local Similarity 98.3%; Pred. No. 1,1e-85;
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MKKALATLIALALPAALAEAGAGFYVOADAHAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAALAEAGAGFYVOADAHAHAKASSLSGAKGSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKKNYKAPSTDFEKLKYSIGASAIYDFDTQSPVKPYLGARLSINRASVDLGSDSF 120
 DB 61 FAVDYTRYKKNYKAPSTDFEKLKYSIGASAIYDFDTQSPVKPYLGARLSINRASVDLGSDSF 120
 QY 121 SQTSGIGLVLTGVSAYAVTPNVDLDAGRYNYIGKVNTRYKNVRSSELSVGVRKF 174
 DB 121 SQTSGIGLVLTGVSAYAVTPNVDLDAGRYNYIGKVNTRYKNVRSSELSVGVRKF 174
 RESULT 3
 AAM04894
 ID AAM04894 standard; Protein; 174 AA.
 AC AAM04894;
 XX
 DT 22-DEC-1996 (first entry)
 XX
 DE Proteinase K resistant N. meningitidis 22 kd surface protein.
 XX
 KW Proteinase K resistant; Neisseria meningitidis;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein;
 XX
 OS Neisseria meningitidis strain b2.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..174
 FT /label= mat_protein
 PN W09629412-A1.
 PD 26-SEP-1996.
 XX
 PF 15-MAR-1996; 96WO-CA00157.
 XX
 PR 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 XX
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39042.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 10; 117pp; English.
 XX
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 XX
 SQ Sequence 174 AA:
 Query Match 95.0%; Score 825; DB 17; Length 174;
 Best Local Similarity 94.3%; Pred. No. 2.1e-82;
 Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNNKAPSTDFEKLKSTGASAIYDFDTQSPKPYLGARLSINRASVDFGSDS 120
 DB 61 FAVDYTRYKNNKAPSTDFEKLKSTGASAIYDFDTQSPKPYLGARLSINRASVDFGSDS 120
 QY 121 SQSTIGLGLVLTGVSAYTPNVLDAGYRNYIGKNTYKNNRSGELSGYRVKF 174
 DB 121 SQSTIGLGLVLTGVSAYTPNVLDAGYRNYIGKNTYKNNRSGELSGYRVKF 174
 RESULT 4
 AAM04892
 ID AAM04892 standard; Protein; 175 AA.
 AC AAM04892;
 XX
 DT 22-DEC-1996 (first entry)
 XX
 DE Proteinase K resistant N. meningitidis 22 kD surface protein.
 XX
 KW Proteinase K resistant; Neisseria meningitidis;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
 XX
 OS Neisseria meningitidis strain MCH88.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..175
 FT /label= mat_protein
 XX
 PN W09629412-A1.
 PD 26-SEP-1996.
 PD
 PF 15-MAR-1996; 96MO-CA00157.
 PF
 XX 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 PI Brodeur BR, Hamel J, Martin D, Rioux C;

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39040.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 8; 117pp; English.
 XX
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
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 SQ Sequence 175 AA:
 Query Match 95.0%; Score 824.5; DB 17; Length 175;
 Best Local Similarity 95.4%; Pred. No. 2.4e-82;
 Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
 QY 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNNK-APSTDFEKLKSTGASAIYDFDTQSPKPYLGARLSINRASVDFGSDS 119
 DB 61 FAVDYTRYKNNKQVSTDFEKLKSTGASAIYDFDTQSPKPYLGARLSINRASVDFGSDS 120
 QY 120 FSQSTIGLGLVLTGVSAYTPNVLDAGYRNYIGKNTYKNNRSGELSGYRVKF 174
 DB 121 FSQSTIGLGLVLTGVSAYTPNVLDAGYRNYIGKNTYKNNRSGELSGYRVKF 175
 RESULT 5
 AAB19895
 ID AAB19895 standard; Protein; 155 AA.
 AC AAB19895;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE Neisseria meningitidis NspA protein.
 XX
 KW NspA; infection; diagnosis; therapy; vaccine; meningococcal B.
 KW Neisseria meningitidis.
 XX
 OS Neisseria meningitidis.
 XX
 FH Key Location/Qualifiers
 FT Region 6..17
 FT /note= "transmembrane beta-strand"
 FT Region 18..26
 FT /note= "surface-exposed connecting loop"
 FT Region 27..37
 FT /note= "transmembrane beta-strand"
 FT Region 40..50
 FT /note= "transmembrane beta-strand"
 FT Region 51..62
 FT /note= "surface-exposed connecting loop"
 FT Region 63..74
 FT /note= "transmembrane beta-strand"
 FT Region 78..88
 FT /note= "transmembrane beta-strand"
 FT Region 89..104
 FT /note= "surface-exposed connecting loop"
 FT Region 105..114
 FT /note= "transmembrane beta-strand"
 FT Region 118..130


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XX OS Synthetic.
XX PN MO9629412-A1.
XX PD 26-SEP-1996.
XX PF 15-MAR-1996; 96WO-CA00157.
XX PR 04-AUG-1995; 95US-0001983.
XX PR 17-MAR-1995; 95US-0406362.
XX PA (IAFB-) IAF BIO VAC INC.
XX PI Brodeur BR, Hamel J, Martin D, Rioux C;
XX DR WPI; 1996-443187/44.
XX PT Neisseria meningitidis antigen, highly conserved between different
XX PT strains - useful for prodn. of antibodies for immunisation against,
XX PT or diagnosis of, N. meningitidis infection
XX PS Claim 24; Page 84; 117pp; English.
XX CC Example 9 describes the epitope mapping of the 22 kD
XX CC N. meningitidis protein. Identification was accomplished
XX CC using 18 overlapping synthetic peptides (AAW04895 to AAW04912).
XX SQ Sequence 25 AA;

Query Match 15.3%; Score 133; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FAVDYTRYKNYKAPSTDFKLSIGA 85
DB 1 FAVDYTRYKNYKAPSTDFKLSIGA 25

RESULT 8
AAU34556
ID AAU34556 standard; Protein; 212 AA.
XX AC AAU34556;
XX DT 14-FEB-2002 (first entry)
XX DE E. coli cellular proliferation protein #137.
XX KM Antisense; prokaryotic cellular proliferation protein;
XX KM antibiotic; antibacterial; drug design.
XX OS Escherichia coli.
XX PN MO200170955-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US09180.
XX PR 21-MAR-2000; 2000US-191078P.
XX PR 23-MAY-2000; 2000US-206848P.
XX PR 26-MAY-2000; 2000US-207727P.
XX PR 23-OCT-2000; 2000US-245278P.
XX PR 27-NOV-2000; 2000US-256258P.
XX PR 22-DEC-2000; 2000US-257931P.
XX PR 16-FEB-2001; 2001US-269308P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ,
XX PI Yamamoto RT, Xu HH;

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DR WPI; 2001-611495/70.
DR N-PSDB; AAS52415.
XX PT New polynucleotides for the identification and development of
XX PT antibiotics, comprise sequences of antisense nucleic acids -
XX PS Example 3; Seq ID No 10149; 511pp; English.
XX CC The invention relates to antisense inhibitors of genes essential to
XX CC prokaryotic cellular proliferation, their use in identifying the
XX CC genes, their use in the discovery of novel antibiotics, the essential
XX CC genes themselves and the encoded proteins. The prokaryotes used are
XX CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
XX CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
XX CC invention is also useful for the identification of potential new targets
XX CC for antibiotic development. The antisense nucleic acids can also be used
XX CC to identify proteins used in proliferation, to express these proteins,
XX CC and to obtain antibodies capable of binding to the expressed proteins.
XX CC The proteins can be used to screen compounds in rational drug discovery
XX CC programmes. The antisense nucleic acid sequence is also useful to screen
XX CC for homologous nucleic acids which are required for cell proliferation in
XX CC a wide variety of organisms. The present sequence represents an
XX CC essential prokaryotic cellular proliferation protein.
XX CC Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic
XX CC format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 212 AA;

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Query Match 10.9%; Score 94.5; DB 22; Length 212;
Best Local Similarity 23.3%; Pred. No. 0.035;
Matches 48; Conservative 29; Mismatches 70; Indels 59; Gaps 10;

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QY 1 MKKALFTLIALA--LPAALAEAGSGFYQADAAHAK-----ASSLSGSAKGRSPRTISAGY 54
DB 1 MKKLVYAALAVVTLTSLGSAFAHDAEGEFMRAGSAIVRPEGAGTLGSLGFSV----- 54
QY 55 RINDLRFADVTRYKNYKA-----PSTDFKLYSIGASAIYDF----- 91
DB 55 -TNNTOGLGFTT-----YMTDNIQVGLLAATPR-HKITRATGDIATVYNNIPRLMAOW 108
QY 92 ---DTQSPVKPYIGARLS-----LNRAVDLGSDFSQTSIGLGYLGSVYAVTPN 140
DB 109 YEGDASSKFRPYGAGINVTFFDNCFNDHGEKAGLSLDKDSWGAGQVGVVDYLNRD 168
QY 141 --VDLDAGRYNNTGKVNTPVKNVRSG 164
DB 169 WLVMMSVWYM-----DIDTANKLIG 189

RESULT 9
AAB47447
ID AAB47447 standard; Protein; 353 AA.
XX AC AAB47447;
XX DT 31-OCT-2001 (first entry)
XX DE MOMP P5.
XX KM surface exposed loop; major outer membrane protein P5; MOMP P5;
XX KM non-typeable H. influenzae; ntlH; LB1(f) peptide; B cell epitope;
XX KM otitis media; sinusitis; conjunctivitis;
XX KM lower respiratory tract infection.
XX OS Haemophilus influenzae.
XX PA Key
XX PI Location/Qualifiers
XX PI 38..57 /label= Loop 1
XX PI /note= "Extracellular domain"
XX FT Domain
XX FT 89..100

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DT	14-FEB-2002	(first entry)	
XX			
DE	Salmonella typhi cellular proliferation protein #143.		
XX			
KW	Antisense; prokaryotic cellular proliferation protein;		
KW	antibiotic; antibacterial; drug design.		
XX			
OS	Salmonella typhi.		
XX			
PN	WO200170955-A2.		
XX			
PD	27-SEP-2001.		
XX			
PF	21-MAR-2001; 2001WO-US09180.		
XX			
PR	21-MAR-2000; 2000US-191078P.		
PR	23-MAY-2000; 2000US-206848P.		
PR	26-MAY-2000; 2000US-207777P.		
PR	23-OCT-2000; 2000US-242578P.		
PR	27-NOV-2000; 2000US-253625P.		
PR	22-DEC-2000; 2000US-257931P.		
PR	16-FEB-2001; 2001US-269308P.		
XX			
PA	(ELIT-) ELITRA PHARM INC.		
XX			
PI	Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;		
PI	Yamamoto RT, Xu HH;		
XX			
DR	WPI: 2001-611495/70.		
XX	N-PSDB; AASS6111.		
PT	New polynucleotides for the identification and development of		
XX	antibiotics, comprise sequences of antisense nucleic acids -		
XX	Example 3; Seq ID No 13845; 511pp; English.		
PS			
XX			
CC	The invention relates to antisense inhibitors of genes essential to		
CC	prokaryotic cellular proliferation, their use in identifying the		
CC	genes, their use in the discovery of novel antibiotics, the essential		
CC	genes themselves and the encoded proteins. The prokaryotes used are		
CC	Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella		
CC	pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The		
CC	invention is also useful for the identification of potential new targets		
CC	for antibiotic development. The antisense nucleic acids can also be used		
CC	to identify proteins used in proliferation, to express these proteins,		
CC	and to obtain antibodies capable of binding to the expressed proteins.		
CC	The proteins can be used to screen compounds in rational drug discovery		
CC	programmes. The antisense nucleic acid sequence is also useful to screen		
CC	for homologous nucleic acids which are required for cell proliferation in		
CC	a wide variety of organisms. The present sequence represents an		
CC	essential prokaryotic cellular proliferation protein.		
CC	Note: The sequence data for this patent did not form part		
CC	of the printed specification, but was obtained in electronic		
CC	format directly from WIPO at		
CC	ftp.wipo.int/pub/published_pct_sequences.		
XX			
SO	Sequence 257 AA:		
XX			
Query Match	10.3%; Score 89.5; DB 22; Length 257;		
Best Local Similarity	21.9%; Pred. No. 0.16;		
Matches 46; Conservative 31; Mismatches 70; Indels 63; Gaps 10			
QY	1 MKKALATLILAL--LPAALAEAGASGYQADAAIAK-----ASSLSGAKGFSPRISAGY 54		
DB	27 MKKTYVALALTLTLGSAFAHAEFFEMRAPPAIVRPTGAGCGTGLHGFED--VS-- 81		
QY	55 RINDLRPAVDYTYKKYKA-----PSTQFKIYSIGASAIYDF----- 91		
DB	82 --NNTQGLHFT-----YMATDNTGVELLAATFPR-HXYGTATGDIATVHLPLPTLMAQW 134		
QY	92 ----DTQSPVKPYIGARLS-----LNRASVDLGGDSFSQTSIGICVLTVGSVAYT- 138		
DB	135 YFGSSSSKVPYGVGVNVTTFEDNDFNDNGKKGTLSDLSFKDSGAAGGVGYDLINRD 194		

Db 51 IGVLRGAAAEFALNSDGFILAPGLAVTMGAKMESLSETTTRHLIQLIPVNAQMRRS-- 108
 QY 60 RFANDYTRYNNKAPSPDFELYSIGASAIYDPTQSPVRYLGLARLSLNRAVDLGSDS 119
 Db 109 -FA-----DNNALISLEAGPYFAYGVAGTIK---TKVAGVTASVDAPFGDNG 149
 QY 120 FSGTSGIGLVLTGVSAYAVTPNVLDAGYRNYIGKVTNK-----NVRSGELSVGRVK 173
 Db 150 YNRFDLGLGLSALSY---DRIYVQIGYEH---GILNMLKADPKTSLRNHDFVGLGVR 203
 QY 174 F 174
 Db 204 F 204

RESULT 13
 AAY34400
 ID AAY34400 standard; Protein; 221 AA.
 AC AAY34400;
 DF 25-AUG-1999 (first entry)
 DE Porphyromonas gingivalis protein PG64.
 KM Porphyromonas gingivalis; PG; periodontal disease; gingivitis;
 OS vaccine; antigenic.
 XX Porphyromonas gingivalis.
 PN WO9929870-A1.
 PD 17-JUN-1999.
 PF 10-DEC-1998; 98W0-AU01023.
 PR 04-AUG-1998; 98AU-0005028.
 PR 10-DEC-1997; 97AU-0000839.
 PR 31-DEC-1997; 97AU-0001182.
 PR 30-JAN-1998; 98AU-0001546.
 PR 10-MAR-1998; 98AU-0002264.
 PR 09-APR-1998; 98AU-0002911.
 PR 23-APR-1998; 98AU-0003128.
 PR 05-MAY-1998; 98AU-0003338.
 PR 22-MAY-1998; 98AU-0003654.
 PR 29-JUL-1998; 98AU-0004917.
 XX (CSLC-) CSL LTD.
 PA Agilus CT, Barr IG, Hocking DM, Margolis MB, Patterson MA;
 PI Ross BC, Rothel LJ, Webb EA;
 DR WPI: 1999-385613/32.
 DR N-PSDB; AAX91618.
 PT Antigenic Porphyromonas gingivalis peptides for preventing
 PT gingivitis
 PS Claim 1; Page 371; 588pp; English.
 CC AAX91536 to AAX91801 encode two hundred and sixty six antigenic
 CC Porphyromonas gingivalis (PG) polypeptide sequences given in AAX34318 to
 CC AAX34583. AAX91802 to AAX91989 represent PCR primers used in the
 CC isolation of the PG polypeptides. The PG polypeptides have antibacterial
 CC activity with a vaccine mechanism of action. The PG polypeptides can be
 CC used as vaccines especially against Porphyromonas gingivalis. Probes can
 CC be used to detect Porphyromonas gingivalis in standard hybridisation
 CC assays. Porphyromonas gingivalis is involved in periodontal disease
 CC especially gingivitis.
 SO Sequence 221 AA;
 Query Match 10.2%; Score 88.5; DB 20; Length 221.

Best Local Similarity 22.1%; Pred. No. 0.17;
 Matches 40; Conservative 35; Mismatches 65; Indels 41; Gaps 8;
 QY 8 LIALPAAA-LAEGACSFYVQADAAHAKASSLSIGAKFSPR-----ISAGYRINDL 59
 Db 68 IGVLRGAAAEFALNSDGFILAPGLAVTMGAKMESLSETTTRHLIQLIPVNAQMRRS-- 125
 QY 60 RFANDYTRYNNKAPSPDFELYSIGASAIYDPTQSPVRYLGLARLSLNRAVDLGSDS 119
 Db 126 -FA-----DNNALISLEAGPYFAYGVAGTIK---TKVAGVTASVDAPFGDNG 166
 QY 120 FSGTSGIGLVLTGVSAYAVTPNVLDAGYRNYIGKVTNK-----NVRSGELSVGRVK 173
 Db 167 YNRFDLGLGLSALSY---DRIYVQIGYEH---GILNMLKADPKTSLRNHDFVGLGVR 220
 QY 174 F 174
 Db 221 F 221

RESULT 14
 AAW68202
 ID AAW68202 standard; Protein; 573 AA.
 AC AAW68202;
 DF 07-OCT-1998 (first entry)
 DE M. catarrhalis strain O35E USP2 antigen.
 KM Moraxella catarrhalis; USP2; antigen; genetic vaccination;
 KM vaccine; otitis media; sinusitis; lower respiratory tract infection;
 KM immunity enhancer; immunoassay reagent.
 OS Moraxella catarrhalis.
 PN WO9828333-A2.
 PD 02-JUL-1998.
 PF 19-DEC-1997; 97W0-US23930.
 PR 20-DEC-1996; 96US-00033598.
 PA (TEXA) UNIT TEXAS SYSTEM.
 PI Aebi C, Cope LD, Fiske MJ, Friedenburt R, Hansen EJ;
 PI Mactiver I;
 DR WPI: 1998-377595/32.
 DR N-PSDB; AAW41342.
 PT New peptide(s) containing the core epitope of Moraxella catarrhalis
 PT USP proteins - useful in, e.g. vaccines to prevent or treat M.
 PT catarrhalis infection, and antibodies for passive immunisation
 PS Claim 24; Pages 138-140; 237pp; English.
 CC This represents a USP2 antigen of Moraxella catarrhalis strain O35E.
 CC Nucleic acid sequences encoding the USP1 and A2 antigens of
 CC M. catarrhalis isolates O35E, O46E, TR24 and TR37 can be used in
 CC genetic vaccination. An antigenic composition or vaccine containing
 CC antigenic peptides from USP1 or USP2 antigens are used to induce an
 CC immune response in mammals against M. catarrhalis and can be used to
 CC treat infections such as otitis media, sinusitis, lower respiratory
 CC tract infections. They can also be used as immunity enhancers for other
 CC bacterial, parasitic or viral antigens, to raise antibodies and as
 CC immunoassay reagents for detecting specific antibodies. The antibodies
 CC are useful for passive immunisation and as immunoassay reagents.
 CC Detection of the epitopic core sequence, by immunoassay or by PCR, is
 CC used to diagnose infection. The USP antigens encoding nucleic acid
 CC sequences are also used to produce recombinant proteins and for screening
 CC for potential anti-M. catarrhalis agents, while their fragments are

CC	useful as diagnostic probes or primers or to isolate variant sequences
XX	
SQ	Sequence 573 AA;

50 Sequence 573 AA;

Query Match	10.28;	Score 88.5;	DB 19,	Length 573;
Best Local Similarity	24.68;	Pred. No. 0.62;		
Matches 42;	Conservative 29;	Mismatches 59;	Indels 41;	Gaps 9;

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QY 19 AEGSAGEVQADA-----AIAKSSSSIS-AKFFSPRIK-GRINDLREAVDYTR 67
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Db 429 ASADTFKFAATADATYTKNGNNAITTKNAKSTIDTGTKVDFGDGRVTLADTKVNAI-----480
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QY 68 YKNKAFTDEKLTSGISASATYEDPDQSPV-----KPLTGLARSLINRASVLDGSDSPQT 123
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 481 -DTRKNAFDORITRILDSKVENGMAMALSLGLEPFIYSYKFN--ATALALGIGSKSAV 535
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 124 SIGIGVLTVSYANTPVNDDAGTFRITRTIGKVTYKKNRSGELSGSVGRVKE 174
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 536 AILGG-----TRVNPNLAEKAG-----AALNLSGN-KKGSYITGVNTE 573
      | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 15

AAW06206
ID AAW68206 standard; Protein; 610 AA.
XX

AC AAW68206;

DT 07-OCT-1998 (first entry)

DE M. catarrhalis strain TTA24 UspA2 antigen

KM Moraxella catarrhalis; USpa1; USpa2; antigen; genetic vaccination;
 KM vaccine; otitis media; sinusitis; lower respiratory tract infection.
 KM Immunity enhancer; Immunoassay reagent.

05 Moraxella catarrhalis.

PN W09828333-A2.

PD 02-JUL-1998.

PF 19-DEC-1997; 97WO-US23930.

PR 20-DEC-1996; 96US-0033598.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Aebi C, Cope LD, Fiske MJ, Fredenburg R, Hansen EJ;
PI Medvet T.

AA WPT. 1000-377505/33
DP

DK N-PSDB; AAV41346
YY

PT New peptide(s) containing the core epitope of Moraxella catarrhalis
PT 50p proteins - useful in, e.g. vaccines to prevent or treat M.
PT catarrhalis infection, and antibodies for passive immunisation
PS
PS Claim 32, Pages 157-159, 237pp. English.

This represents a *UspA2* antigen of *Moraxella catarrhalis* strain TPA24. Nucleic acid sequences encoding the *UspA1* and *A2* antigens of *M. catarrhalis* isolates 035F, 046F, TPA24 and TPA37 can be used in genetic vaccination. An antigenic composition or vaccine containing antigenic peptides from *UspA1* or *UspA2* antigens are used to induce an immune response in mammals against *M. catarrhalis* and can be used to treat infections such as otitis media, sinusitis, lower respiratory tract infections. They can also be used as immunity enhancers for other bacterial, parasitic or viral antigens, to raise antibodies and as immunoassay reagents for detecting specific antibodies. The antibodies are useful for passive immunisation and as immunoassay reagents. Detection of the epitopic core sequence, by immunoassay or by PCR, is used to diagnose infection. The *usp* antigens encoding nucleic acid sequences are also used to produce recombinant proteins and for screening

CC for potential anti-M. catarrhalis agents, while their fragments are
CC useful as diagnostic probes or primers or to isolate variant sequences
VV

CC

SQ	Sequence	610 AA;
1
2
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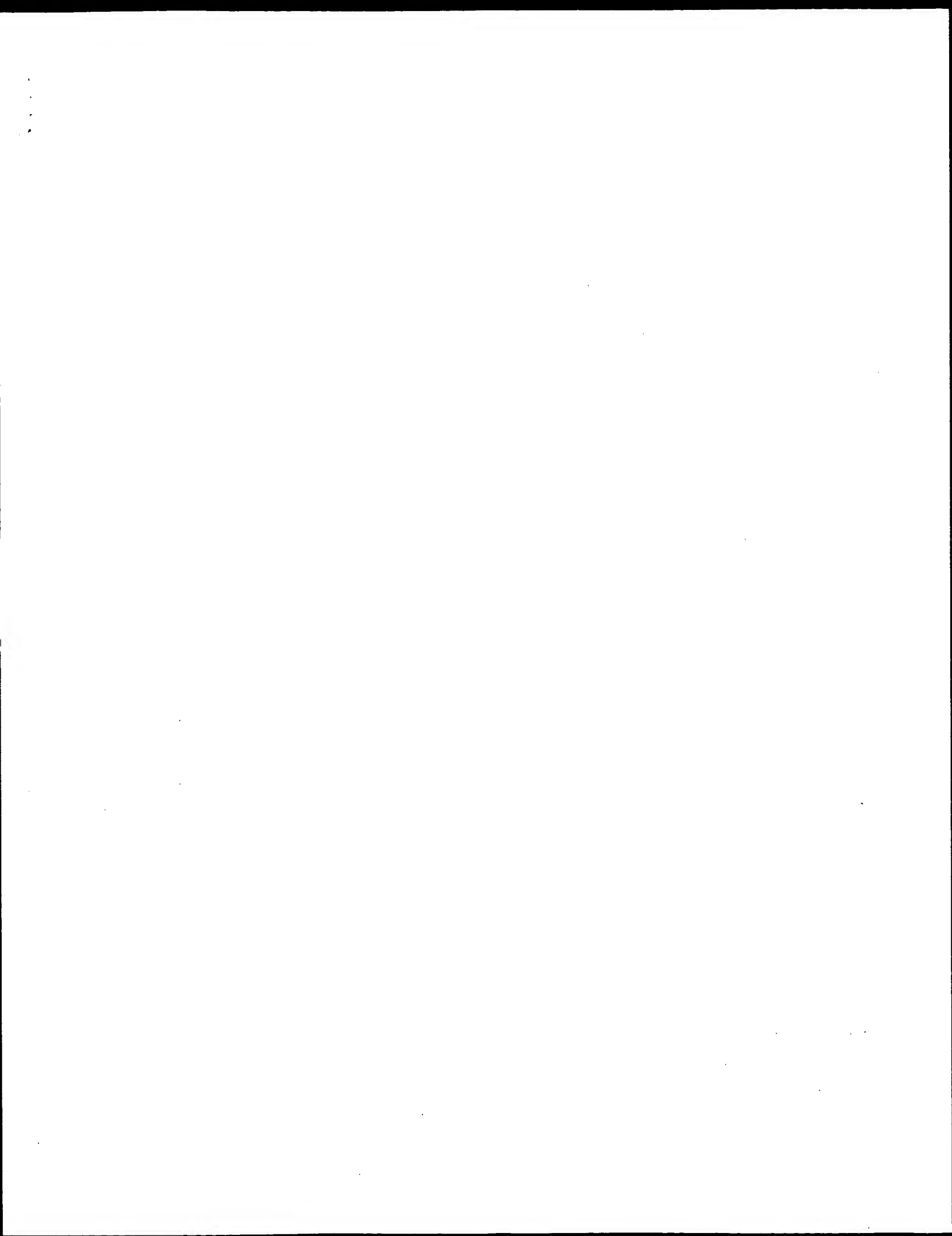
Query Match	10.1%	Score 88;	DB 19;	Length 610;
Best Local Similarity	26.0%	Pred. No. 0.76;		
Matches 45;	Conservative 22;	Mismatches 54;	Indels 52;	Gaps 9.

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QY 19 AEGASFEYVOADA-----AAAKSSSSIGS-AGGESPISA-GYRIN--DLREAVDY 65
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 473 ASADTFKAATADALITKNGNAITLTKNAKSTITDLGTRKVDGDFGRTALDTKNAFDGTTALD 533
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 66 TRKKN-----YKAPSTDFKLVSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDFS 121
      : : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 533 SKYENGMQAALSLGFLPYSYGKF-----NNTAALGGYSGKS 570
      : : | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 122 QTSIGLGLTVGSYAFTPNVDLDAGRYRNTYIGKVTNTVKNVRSGLSVGYRVEF 174
      : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 571 AVAIGAG-----YRVNNINLAFKAG-----AALINTSGN-KKGGSNTIGYNNVEF 610
      : : | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Search completed: October 28, 2002, 16:00:36
Job time : 26.7145 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:58:54 ; Search time 9.48637 Seconds
(without alignments)
448.017 Million cell updates/sec

Title: US-09-684-883-2
Perfect score: 868
Sequence: 1 MKKALATLIALPAALAE.....VNTWKVRSGLSVGRVKF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	868	100.0	174	4	US-08-913-362-2
2	854	98.4	174	4	US-08-913-362-6
3	838.5	96.6	175	4	US-08-913-362-30
4	825	95.0	174	4	US-08-913-362-8
5	824.5	95.0	175	4	US-08-913-362-4
6	135	15.6	170	1	US-08-127-499A-20
7	135	15.6	170	1	US-08-482-847-20
8	133	15.3	25	4	US-08-913-362-26
9	88.5	10.2	573	4	US-09-336-447A-3
10	88	10.1	359	1	US-08-457-997B-2
11	88	10.1	359	3	US-08-467-722A-2
12	88	10.1	610	4	US-09-336-447A-11
13	88	10.1	624	4	US-09-336-447A-7
14	88	10.1	889	4	US-09-336-447A-15
15	87	10.0	16	4	US-08-913-362-15
16	85	9.8	568	4	US-08-913-362-15
17	82	9.4	433	2	PCT-US95-13749-5
18	81	9.3	15	4	US-08-883-515-2
19	79	9.1	15	4	US-08-913-362-23
20	78.5	9.0	286	1	US-08-382-184-3
21	78.5	9.0	286	2	US-08-641-356-3
22	78.5	9.0	286	4	US-09-132-528-4
23	78.5	9.0	286	4	US-08-875-494-3
24	78.5	9.0	286	4	US-09-599-366-4
25	78.5	9.0	325	1	US-08-382-184-2
26	78.5	9.0	325	2	US-08-641-356-2
27	78.5	9.0	325	4	US-09-132-528-2

28	78.5	9.0	325	4	US-09-132-528-3	Sequence 3, Appl
29	78.5	9.0	325	4	US-08-875-494-2	Sequence 2, Appl
30	78.5	9.0	325	4	US-09-599-366-2	Sequence 2, Appl
31	78.5	9.0	325	4	US-09-599-366-3	Sequence 2, Appl
32	78.5	9.0	332	4	US-08-818-112-53	Sequence 53, Appl
33	78.5	9.0	332	4	US-08-818-111-53	Sequence 53, Appl
34	78.5	9.0	332	4	US-09-056-555-53	Sequence 53, Appl
35	78.5	9.0	802	4	US-09-056-556-214	Sequence 53, Appl
36	78.5	9.0	15	4	US-08-913-362-14	Sequence 214, App
37	78	9.0	15	4	US-08-913-362-16	Sequence 14, Appl
38	77	8.9	15	4	US-08-913-362-11	Sequence 16, Appl
39	77	8.9	15	4	US-08-913-362-13	Sequence 11, Appl
40	77	8.9	2123	4	US-08-968-685A-10	Sequence 10, Appl
41	76	8.8	15	4	US-08-913-362-17	Sequence 17, Appl
42	76	8.8	15	4	US-08-913-362-22	Sequence 12, Appl
43	76	8.8	15	4	US-08-913-362-24	Sequence 24, Appl
44	76	8.8	207	2	US-08-381-881-6	Sequence 6, Appl
45	76	8.8	207	4	US-09-281-221-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-913-362-2
Sequence 2, Application US/08913362
Patent No. 6287574
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-913-362-2
Query Match 100.0%, Score 868, DB 4, Length 174.

Best Local Similarity 100.0%; Pred. No. 3e-93;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNKAPSTDFKLYSIGASAIYDFIQSPVKPYLGARLSLNRAVDLGSDSF 120
DB 61 FAVDYTRYKNKAPSTDFKLYSIGASAIYDFIQSPVKPYLGARLSLNRAVDLGSDSF 120
QY 121 SQTSGIGLVLTGVSYAVTPNVDLDAGYRYNYIGKVTYKKNVRSGLSVGRVVF 174
DB 121 SQTSGIGLVLTGVSYAVTPNVDLDAGYRYNYIGKVTYKKNVRSGLSVGRVVF 174

RESULT 2

US-08-913-362-6
; Sequence 6, Application US/08913362
; Patent No. 6287574

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 04/7998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-913-362-6

Query Match 98.4%; Score 854; DB 4; Length 174;
Best Local Similarity 98.3%; Pred. No. 1.3e-91;
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNKAPSTDFKLYSIGASAIYDFIQSPVKPYLGARLSLNRAVDLGSDSF 120
DB 61 FAVDYTRYKNKAPSTDFKLYSIGASAIYDFIQSPVKPYLGARLSLNRAVDLGSDSF 120

QY 121 SQTSGIGLVLTGVSYAVTPNVDLDAGYRYNYIGKVTYKKNVRSGLSVGRVVF 174
DB 121 SQTSGIGLVLTGVSYAVTPNVDLDAGYRYNYIGKVTYKKNVRSGLSVGRVVF 174

RESULT 3

US-08-913-362-30
; Sequence 30, Application US/08913362
; Patent No. 6287574

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 04/7998/0128
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TELEFAX: (202)672-5399

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-913-362-30

Query Match 96.6%; Score 838.5; DB 4; Length 175;
Best Local Similarity 97.1%; Pred. No. 8.1e-90;
Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNKAPSTDFKLYSIGASAIYDFIQSPVKPYLGARLSLNRAVDLGSDS 119
DB 61 FAVDYTRYKNKAPSTDFKLYSIGASAIYDFIQSPVKPYLGARLSLNRAVDLGSDS 120

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DB 120 SQTSGIGLVLTGVSYAVTPNVDLDAGYRYNYIGKVTYKKNVRSGLSVGRVVF 174

[illegible]

REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
STRAIN: 6088
US-08-913-362-26

Query Match 15.3%; Score 133; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FAVDYTRYKKNYKAPSTDFKLYSIGA 85
1 FAVDYTRYKKNYKAPSTDFKLYSIGA 25

RESULT 9
US-09-336-447A-3
Sequence 3, Application US/09336447A
Patent No. 6310190
GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 3
LENGTH: 573
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-09-336-447A-3

Query Match 10.2%; Score 88.5; DB 4; Length 573;
Best Local Similarity 24.6%; Pred. No. 0.084;
Matches 42; Conservative 29; Mismatches 59; Indels 41; Gaps 9;

QY 19 AEGASGFYVQADA-----AHAKASSSLGS-AKGFSPRISA-GYRINDLFAVDYTR 67
DB 429 ASADTFAATADAITKNGAIAITKMAKSTDLSTKYDGFEGRTALDPTKYNAL----- 480

QY 68 YKNYKAPSTDFKLYSIGASAIYDFDQSPV---KPYLGARLSLNKASVDLGSDFSQGT 123
DB 481 --DFTKNAPDFGRITALDSKVENGMMAQALSGLFQPSYSGKEN--ATFALDGYGSKSAV 535

QY 124 SIGLVLTVGVSAVTPNVLDAGYRNYTGKNTYKKNVAGSELGSGVRYKF 174
DB 536 AIGAG-----YRVNPNLAFFKAG-----MAINTSGN-KKGSYNGIVNVEF 573

RESULT 10
US-08-457-997B-2
Sequence 2, Application US/08457997B
Patent No. 576608
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,997B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Colrick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-457-997B-2

Query Match 10.1%; Score 88; DB 1; Length 359;
Best Local Similarity 22.7%; Pred. No. 0.048;
Matches 52; Conservative 29; Mismatches 84; Indels 64; Gaps 11;

QY 1 MKKALATLIALALPAAALABA---SGFYVQADA---HAKSSSLGS-AKGFSPRISAG 53
DB 1 MKKALALVAGLAASVAVQAAPQENTFYAGVAKAGSGSFHDGINNCAIKGLSS-NG 59

QY 54 YRINDLRFVAVDYTRYKKNYKAPSTDFKLYSIGASAIYDFD-----TQSPYKPYL----- 102
DB 60 YRRNTFTYGV---FGGYQLINOD-----NFGLAHELGYDDPGRAKLREAGKPRAKHTNNG 111

QY 103 ARLSLNKASVDLGSDFSQGTSLGL-----GVL-TGVAS 134
DB 112 AYLKLSGEVLDGLDLYGKAGVALVSDYKFEYEDANGTRDHHKGRHTARASGLFAVGA 171

QY 135 YAVTPNVLDAGY-----RYNTYGVNRYKKNYRS--GELSGVRYKF 174
DB 172 YAVPELAVRLEYQMLTRVCKYRPQDKPNTAINYNPWIGCINAGISYRF 220

RESULT 11
US-08-467-722A-2
Sequence 2, Application US/08467722A
Patent No. 6030626
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/467,722A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Goltick, Mary E.
; REGISTRATION NUMBER: 34,829
; REFERENCE/DOCKET NUMBER: 22727/00102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 622-8458
; TELEFAX: (216) 241-0816
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-722A-2

Query Match
Best Local Similarity 10.1%; Score 88; DB 3; Length 359;
Matches 52; Conservative 29; Mismatches 84; Indels 64; Gaps 11;

QY 1 MKKALATLIALPALAALAGA---SGFYQADAA---HAKASSLSGSKGSPRISAG 53
DB 1 MKKTAIALVAGLAASVAQAADQENTFYAGVRAGOGSGFDGINNGALTKKGLSSS-NYG 59
QY 54 YRINDLFAVDYTRKYKAPSTDFKLYSGASAIYDFD-----TQSPYKPYL-----G 102
DB 60 YRRMTFTYGV---FGGYQLNDD---NFGLAELGYDDFGAKLREAGKPRKAKRTNNG 111
QY 103 ARLSLNASVDLGSDSFSQTSIGL-----GVL-TGVS 134
DB 112 AYLSLKGSEYELDGLDYGKAGVALYRSDYKFEYEDANGTRDHKKRHRTARASGLFAVGA 171
QY 135 YAVLPNDLDAGY-----RYNIGKVNTKKNVRS--GELSGVRYKF 174
DB 172 YAVLPDLAHLRYQLWLTTRVGKTRPDKPTAINPWTGICINAGISYRF 220

RESULT 12
US-09-336-447A-11
; Sequence 11, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/336,447A
; CURRENT FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-11

Query Match
Best Local Similarity 10.1%; Score 88; DB 4; Length 610;
Matches 45; Conservative 22; Mismatches 54; Indels 52; Gaps 9;

QY 19 AEGASGTYVQADA-----AHAKASSLSGS-ANGFSPRISA-GYRIN--DLRFADV 65
DB 473 ASADTRKFAATADAITKGNNAITKNAKSITDGLTKYVDFGFRVATLDTKYNAFGRITLAD 532
QY 66 TRYKN-----YKAPSTDFKLYSGASAIYDFDTPQSPVKPYLGLARLSLNASVDLGSDSFS 121
DB 533 SKYENGMAQAALSLGLFPISYVKF-----NATAALGGYGSKS 570
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QY 122 QTSIGLVLTGVSAVTPNDLDAGRYNYIGKVTYKKNVRSSELGSGVRYKF 174
DB 571 AVAIGAG-----YKVNPLAFKAG-----AAINTSGN-KKGSYINIGVNTYEF 610

RESULT 13
US-09-336-447A-7
; Sequence 7, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/336,447A
; CURRENT FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 624
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-7

Query Match
Best Local Similarity 10.1%; Score 88; DB 4; Length 624;
Matches 45; Conservative 22; Mismatches 54; Indels 52; Gaps 9;

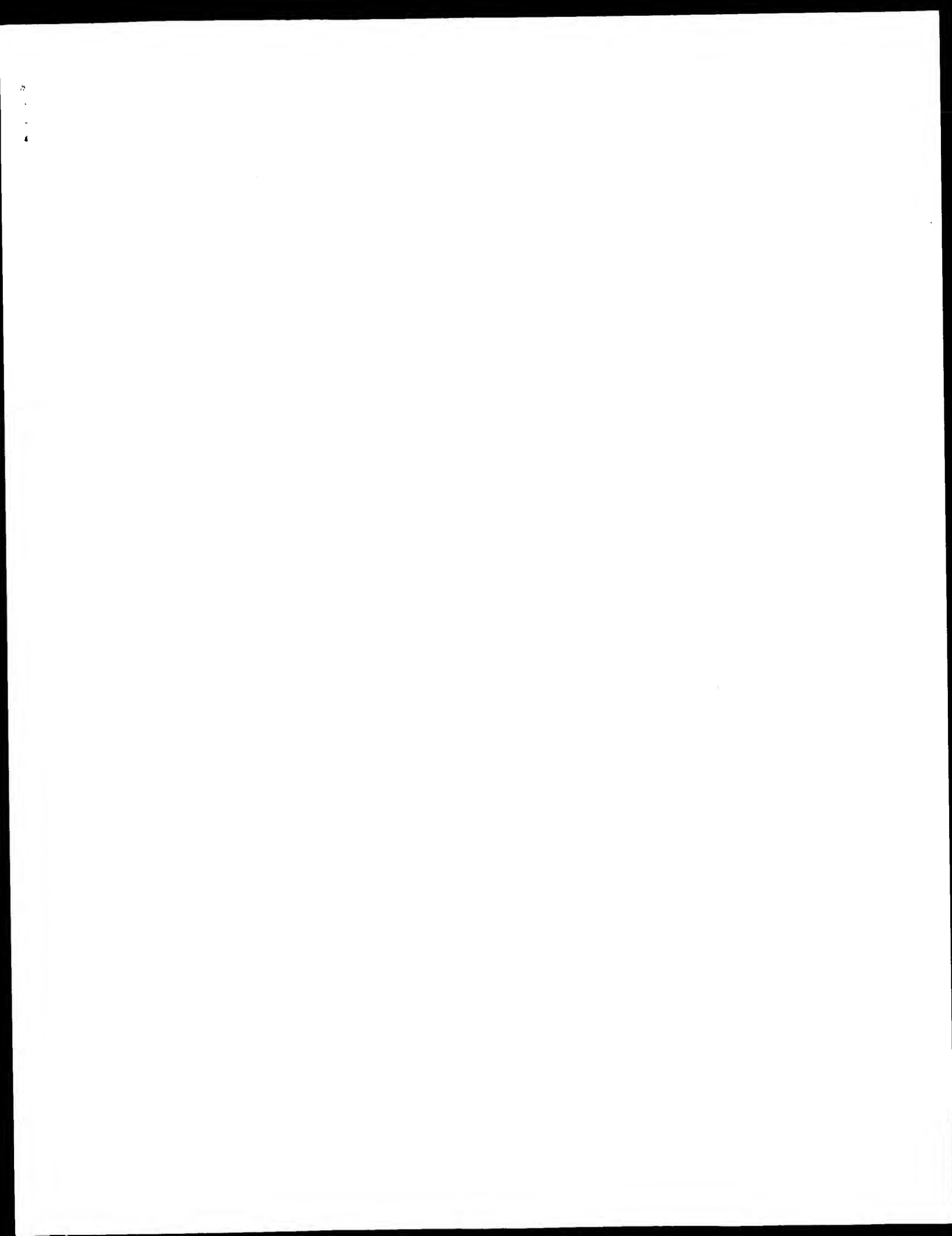
QY 19 AEGASGTYVQADA-----AHAKASSLSGS-ANGFSPRISA-GYRIN--DLRFADV 65
DB 487 ASADTRKFAATADAITKGNNAITKNAKSITDGLTKYVDFGFRVATLDTKYNAFGRITLAD 546
QY 66 TRYKN-----YKAPSTDFKLYSGASAIYDFDTPQSPVKPYLGLARLSLNASVDLGSDSFS 121
DB 547 SKYENGMAQAALSLGLFPISYVKF-----NATAALGGYGSKS 584
DB 585 AVAIGAG-----YKVNPLAFKAG-----AAINTSGN-KKGSYINIGVNTYEF 624

RESULT 14
US-09-336-447A-15
; Sequence 15, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/336,447A
; CURRENT FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 889
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-15

Query Match
Best Local Similarity 10.1%; Score 88; DB 4; Length 889;
Matches 45; Conservative 22; Mismatches 54; Indels 52; Gaps 9;
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Search completed: October 28, 2002, 16:04:18
Job time : 11.4864 secs

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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:58:04 ; Search time 12.4821 Seconds

(without alignments)
1339,485 Million cell updates/sec

Title: us-09-684-883-2

Perfect score: 868

Sequence: 1 MKKALATLIALALPAAALAE.....VNTYKNVSGELSGVGRVKE 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : PIR_71:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	864	99.5	174	2	outer membrane pro
2	854	98.4	174	2	outer membrane pro
3	244.5	28.2	261	2	opacity protein op
4	242	27.9	260	2	opacity protein op
5	241.5	27.8	338	2	opacity protein op
6	241	27.8	258	2	opacity protein op
7	241	27.8	260	1	opacity protein op
8	240.5	27.7	237	2	opacity protein op
9	240.5	27.7	257	2	opacity protein op
10	239	27.5	266	2	opacity protein op
11	238	27.4	258	2	opacity protein op
12	237	27.3	254	2	opacity protein op
13	237	27.3	270	2	opacity protein op
14	236.5	27.2	268	1	opacity protein P.
15	236	27.2	283	2	opacity protein P.
16	235.5	26.8	234	2	opacity protein op
17	235.5	26.8	282	2	opacity protein op
18	232	26.7	234	2	opacity protein op
19	232	26.7	234	2	opacity protein op
20	231	26.6	233	2	opacity protein op
21	226	26.0	234	1	opacity protein V2
22	226	26.0	234	2	opacity protein op
23	226	26.0	238	2	opacity protein op
24	226	26.0	261	2	opacity protein op
25	224.5	25.9	243	2	opacity protein op
26	221	25.5	248	2	opacity protein op
27	219	25.2	178	2	opacity protein op
28	217	25.0	178	2	opacity protein op
29	215	24.8	239	2	opacity protein op

30	205.5	23.7	247	2	S28627	opacity protein op
31	203.5	23.4	214	2	S44706	opacity protein op
32	189.5	21.8	235	2	S44707	opacity protein op
33	180	20.7	121	2	I64187	opacity protein ho
34	150.5	17.3	210	2	S77337	opacity protein op
35	141	16.2	187	2	S20044	opacity protein op
36	135	15.6	168	2	S08513	opacity protein-re
37	135	15.6	170	2	T10256	opacity protein-re
38	132	15.2	239	2	AH0541	outer surface prot
39	129.5	14.9	281	2	AH3012	probable outer mem
40	129.5	14.9	284	2	G98271	probable outer mem
41	126.5	14.6	70	2	P64066	opacity protein op
42	126.5	14.6	201	2	S16286	opacity protein op
43	126	14.5	192	2	S44712	heat resistant agg
44	122	14.1	284	2	AG3556	heat resistant agg
45	121.5	14.0	264	2	I54668	heat resistant agg

ALIGNMENTS

RESULT 1
G81174
outer membrane protein NsgA NMB0663 [imported] - Neisseria meningitidis (strain MC58
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #ext_change 19-Jan-2001
C:Accession: G81174
R:Retelling, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizsa, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: AB1000; MIMD:20175755
A:Accession: G81174
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-174 <RET>
A:Cross-references: GB:AE002420; GB:AE002098; NID:g7225876; PIDN:AAFA1081.1; PID:g722
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0663

Query Match 99.5%; Score 864; DB 2; Length 174;
Best Local Similarity 99.4%; Pred. No. 1.4e-70;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKALATLIALALPAAALAGASGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDR 60
Db 1 MKKALATLIALALPAAALAGASGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDR 60

QY 61 FAVYTRYKNVKNKAPSTDFKLYSGASAIYDFQSPYKPYLGARLSINRASYDLGSDSF 120
Db 61 FAVYTRYKNVKNKAPSTDFKLYSGASAIYDFQSPYKPYLGARLSINRASYDLGSDSF 120

QY 121 SQTSGIGLVLTGSYAVTPNVDADAGYRNYIGKRVTKNVRSGELSGVGRVKE 174
Db 121 SQTSGIGLVLTGSYAVTPNVDADAGYRNYIGKRVTKNVRSGELSGVGRVKE 174

RESULT 2
B81932
outer membrane protein NMA0862 [imported] - Neisseria meningitidis (strain Z2491 sero
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #ext_change 02-Feb-2001
C:Accession: B81932
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491 A:Reference number: AB1775; MIMD:20222556
A:Accession: B81932
A>Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-174 <P>
 A:Cross-references: GB:AL162754; GB:AL157959; NID:q7379424; PIDN:CAB84143.1; PID:q737957
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: nspa; NMA0862

Query Match 98.4%; Score 854; DB 2; Length 174;
 Best Local Similarity 98.3%; Pred. No. 1, le-69;
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALALPAAALAGAGSYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 Db 1 MKKALATLIALALPAAALAGAGSYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 QY 61 FAVDYTKKYNKAPSTDFKIXSGASAIYDPQSPKPYLGLARLSINRASVLDGSDSF 120
 Db 61 FAVDYTKKYNKAPSTDFKIXSGASAIYDPQSPKPYLGLARLSINRASVLDGSDSF 120

QY 121 SQTSGIGLVLTGVSYAVTPNVDLAGRYNYIKGKNTYKKNVRSGLSGVRKVF 174
 Db 121 SQTSGIGLVLTGVSYAVTPNVDLAGRYNYIKGKNTYKKNVRSGLSGVRKVF 174

RESULT 3

Opacity protein opak precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
 N:Alternate names: outer membrane protein opak
 C:Species: Neisseria gonorrhoeae
 A:Variety: strain MS11

C:Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
 C:Accession: S16610
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, M.O. Microbiol. 5, 1889-1901, 1991
 A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam1

A:Reference number: S16610; MUID:92114767

A:Accession: S16610

A:Molecule type: DNA

A:Residues: 1-261 <BHA>

A:Cross-references: EMBL:X52364

A:Experimental source: strain MS11, variant 4.8

A>Note: the authors did not translate the sequence for the signal peptide

A>Note: expression of opacity proteins is regulated by the number of translated repeat

A:Note: repeats place the start codon in frame with the rest of the protein

C:Genetics:

A:Gene: opak

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>

F:24-261/Product: opacity protein opak #status predicted <MAT>

F:34-42/Domain: transmembrane #status predicted <TM1>

F:43-75/Domain: extracellular #status predicted <EXT1>

F:51-61/Region: semivariable region

F:76-84/Domain: transmembrane #status predicted <TM2>

F:89-95/Domain: transmembrane #status predicted <TM3>

F:96-104/Domain: extracellular #status predicted <EXT2>

F:102-129/Region: hypervariable region HV1

F:135-149/Domain: transmembrane #status predicted <TM4>

F:155-165/Domain: transmembrane #status predicted <TM5>

F:166-212/Domain: extracellular #status predicted <EXT3>

F:171-218/Region: hypervariable region HV2

F:213-225/Domain: transmembrane #status predicted <TM6>

F:229-237/Domain: transmembrane #status predicted <TM7>

F:238-252/Domain: extracellular #status predicted <EXT4>

F:253-261/Domain: transmembrane #status predicted <TM8>

Query Match 28.2%; Score 244.5; DB 2; Length 261;

Best Local Similarity 29.9%; Pred. No. 1, le-14;

Matches 73; Conservative 26; Mismatches 58; Indels 87; Gaps 10;

QY 15 AAALAEAG-ASGFYVQADAAHAKA-----SSLSGAKG-----FSPRI 50
 Db 21 AQAASENGNGPIVQADLAIAERITHDYPEPIGAKKGTITISVDFRNKITHSHPRV 80

QY 51 SAGYRINDLRFAVDYTRYKNY-----KAPSTDEK-----LYS 82

Db 81 SVGYDFGCMRIADYARRRKNNKYSVSIKELLRNKNGNRTDLKAEENGTFHAAVS 140

QY 83 IGASAIYDFDQSPVKPFLGARLSLN--RASVD-----LGG-----116

Db 141 LGLSAVYDFKLNDRKPIGARVAAGHRHSDTKTEVTITLHGGTTPYPPGKNT 200

QY 117 -----SDFSQTSIGLVLTGVSYAVTPNVDLAGRYNYIKGKNTYKKNVRSGLSGV 170

Db 201 QNAHRESDSIR--VGLGAVAGVGDIDTPNLTLAGRYHYHWGRLNTR--FKTHEASLGV 257

QY 171 RYKF 174

Db 258 RYKF 261

RESULT 4

Opacity protein opak precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
 N:Alternate names: outer membrane protein opa58
 C:Species: Neisseria gonorrhoeae
 A:Variety: strain MS11

C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 26-Aug-1999
 C:Accession: S16611; S36345; S28624
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc M.O. Microbiol. 5, 1889-1901, 1991
 A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f

A:Reference number: S16610; MUID:92114767

A:Accession: S16611

A:Molecule type: DNA

A:Residues: 1-260 <BHA>

A:Cross-references: EMBL:X52371

A:Experimental source: strain MS11, variant 4.8

A>Note: the authors did not translate the sequence for the signal peptide

A>Note: expression of opacity proteins is regulated by the number of translated repea

A>Note: repeats place the start codon in frame with the rest of the protein

C:Genetics:

A:Gene: opak

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>

F:24-260/Product: opacity protein opak #status predicted <MAT>

F:34-42/Domain: transmembrane #status predicted <TM1>

F:43-74/Domain: extracellular #status predicted <EXT1>

F:51-60/Region: semivariable region

F:75-83/Domain: transmembrane #status predicted <TM2>

F:88-94/Domain: transmembrane #status predicted <TM3>

F:95-133/Domain: extracellular #status predicted <EXT2>

F:101-128/Region: hypervariable region HV1

F:134-148/Domain: transmembrane #status predicted <TM4>

F:154-164/Domain: transmembrane #status predicted <TM5>

F:165-211/Domain: extracellular #status predicted <EXT3>

F:217-217/Region: hypervariable region HV2

F:212-224/Domain: transmembrane #status predicted <TM6>

F:229-236/Domain: transmembrane #status predicted <TM7>

F:237-251/Domain: extracellular #status predicted <EXT4>

F:252-260/Domain: transmembrane #status predicted <TM8>

Query Match 27.9%; Score 242; DB 2; Length 260;

Best Local Similarity 29.5%; Pred. No. 2, le-14;


```
OY      117 -----SDSFQSTIGLGYLTGVSYAVTPVDIDACRYNICKVTF 158  
                ||| : ||| : || :||| : ||| | ||| ||| : ||  
Db      186 GTTPTTVYECKNTQDAHRESDSIR--VGIGAAGVGCIDITPFLTLADGRITHMGRLNT 243
```

OY 159 KNVRSGELSVGVRKE 174
 : : : | : | : | : |
Db 244 R-FKTHEASLGVRNF 258

RESULT 7

KONHO

opacity protein opac precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

N.Alternate names: opacity protein V0; triosephosphate dehydrogenase

C.Species: Neisseria gonorrhoeae

A.Variety: strain MS11

C.Date: 31-Mar-1989 #sequence revision 17-Oct-1997 #text_change 16-Jul-1999

C.Accession: S16618; A24429; S36328; S28621

R.Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnljg, F.; Stern, A.; Kupsch,
Mol. Microbiol. 5, 1889-1901, 1991

A.Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a famlly
A.Reference number: S16610; MUID:92114767

A.Molecule type: DNA

A.Residues: 1^260 <BNR>

A.Cross-references: EMBL:X52370

A.Experimental source: Strain MS11, variant 4.8

A.Note: the authors translated the codon CCA for residue 32 as Thr

A>Note: the authors did not translate the sequence for the signal peptide
of repeats place the start codon in frame with the rest of the protein

R.Stern, A.; Brown, M.; Nickel, P.; Meyer, T.F.
Cell 47, 61-71, 1986

A>Title: Opacity genes in Neisseria gonorrhoeae: control of phase and antigenic variation
A.Reference number: A90887; MUID:87002493

A.Accession: A24429

A.Molecule type: DNA

A.Residues: 25-260 <STE>

A>Note: this protein is synthesized as a precursor; however, the authors are uncertain a
nencing

R.Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.,
EMBO J. 12, 641-650, 1993

A>Title: Variable opacity (opa) outer membrane proteins account for the cell tropisms d
A.Reference number: S36328; MUID:93178439

A.Accession: S36328

A>Status: preliminary

A.Molecule type: DNA

A.Residues: 25-260 <KP>

A.Cross-references: EMBL:Z18927; NID:g49323; PIDN:CAA79360.1; PID:g940789
R.Meyer, T.F.
submitted to the EMBL Data Library, November 1992

A.Reference number: S28617

A.Accession: S28621

A.Molecule type: DNA

A.Residues: 25-260 <MEY>

A.Cross-references: EMBL:Z18927; NID:g49323; PIDN:CAA79360.1; PID:g940789
C.Genetics:

A:Superfamily: opacity protein

C.Keywords: cell surface component; transmembrane protein

F:1-11,12-24/Domains: signal sequence (fragments) #status predicted <SIG>
F:25-260/Product: opacity protein opac #status predicted <MAT>
F:35-43/Domains: transmembrane #status predicted <TM1>
F:44-75/Domains: extracellular #status predicted <EXT1>
F:52-61/Region: semivariable region
F:76-84/Domains: transmembrane #status predicted <TM2>
F:89-95/Domains: transmembrane #status predicted <TM3>
F:96-134/Domains: extracellular #status predicted <EXT2>
F:102-129/Region: hypervariable region HV1
F:135-149/Domains: transmembrane #status predicted <TM4>
F:155-165/Domains: transmembrane #status predicted <EXT3>
F:166-211/Domains: extracellular #status predicted <EXT3>
F:171-217/Region: hypervariable region HV2
F:212-224/Domains: transmembrane #status predicted <TM6>

```

F:228-236/Domain: transmembrane #status predicted <TM7>
F:237-251/Domain: extracellular #status predicted <EXT4>
F:252-260/Domain: transmembrane #status predicted <TM8>

Query Match      27.8%; Score 241; DB 1; Length 260;
Best Local Similarity 28.8%; Pred. No. 2,6e-14;
Matches 72; Conservative 30; Mismatches 64; Indels 84; Gaps 9;

QY 6 ATLLALPALAALGASGFYQADPAHA-----KASSLGSKAKGS----- 47
      ::::: ||| ||| ||| ||| |||
Db 14 SSLLESSAAQAASECGRGYPQADLAAYEHITHDYKRPDPSPGKISTVSDFERNIRT 73
      48 ----PRISAGYRINDLRFADVTRY-----KKNKAPSTD-- 77
      ||::| ||| ||| ||| |||
Db 74 HSHHRVSVSGYDFGCGMRITADYARKRKMSDNKYSISIKMRVHKHNSRNKILKTNOENG 133
      ||::| ||| ||| ||| |||
QY 78 --FKYISGASAIYDPFQSPYKPYLGARLSIN--RASVD-----LGG- 116
      ::| ||| ||| ||| ||| |||
Db 134 SFHVAVSLGLAISITFOJINDKFRPYIGARVAAGHRHSIDSTFKITGLTSTPGIMSGV 193
      ::| ||| ||| ||| ||| |||
QY 117 -----SDPSQSIIGLGVLTGSYAVFPNVNLDGVRNYTGKXNTVYNSG 164
      ||| ::| ||| ||| ::| ||| ||| ||| ||| ||| |||
Db 194 YVLRPPGAKHRSDSIRR--VELGIYIAGVGFDITPKLTIDAGCYRIHNMGRLENTR-FKTH 250
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 165 ELISVGRVKE 174
      ||| ||| ||| |||
Db 251 EASLGVRVRE 260

RESULT 8
S36343
opacity protein opa57 - Neisseria gonorrhoeae (strain MS11) (fragment)
N.Alternate names: outer membrane protein opa57
C.Species: Neisseria gonorrhoeae
A.Variety: strain MS11
C.Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C.Accession: S36343; S28626
R.Kupsch, E.W.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
EMBO J. 12, 641-650, 1993
A.Title: Variable opacity (opa) outer membrane proteins account for the cell tropisms
A.Reference number: S36328; MUID:93178439
A.Accession: S36343
A.Molecule type: DNA
A.Residues: 1-237 <KUP>
A.Cross-references: EMBL:Z18935; NID:q49331; PIDN:CAV9368.1; PID:q940797
A.Experimental source: strain MS11, variant F3
A.Note: expression of opacity proteins is regulated by the number of translated repeats
of repeats Place the start codon in frame with the rest of the protein
C.Genetics:
A.Gene: opa57
C.Superfamily: opacity protein
C.Keywords: cell surface component; transmembrane protein
F:1-237/Product: opacity protein opa57 #status predicted <MAT>
F:11-19/Domain: transmembrane #status predicted <TM1>
F:20-51/Domain: extracellular #status predicted <EXT1>
F:28-37/Domain: semivariable region
F:52-60/Domain: transmembrane #status predicted <TM2>
F:65-71/Domain: transmembrane #status predicted <TM3>
F:72-110/Domain: extracellular #status predicted <EXT2>
F:78-105/Region: hypervariable region HVI
F:111-125/Domain: transmembrane #status predicted <TM4>
F:131-141/Domain: transmembrane #status predicted <TM5>
F:142-188/Domain: extracellular #status predicted <EXT3>
F:147-194/Region: hypervariable region HV2
F:189-201/Domain: transmembrane #status predicted <TM6>
F:205-213/Domain: transmembrane #status predicted <TM7>
F:214-228/Domain: extracellular #status predicted <EXT4>
F:229-237/Domain: transmembrane #status predicted <TM8>

Query Match      27.7%; Score 240.5; DB 2; Length 237;
Best Local Similarity 29.6%; Pred. No. 2.6e-14;
Matches 71; Conservative 26; Mismatches 58; Indels 85; Gaps 9;

```

110
110
110

QY 153 GKVNIVKNRSGELSGVRYKF 174

```

      |::      :      :: | |::|| :|
Db  246 GRLENTN-FTHEASLGVRFR 266

```

RESULT 11

S08514
opacity protein-related protein OPM1 precursor - *Neisseria meningitidis* (strain C1938)
N:Alternate names: outer membrane protein class 5
C:Species: *Neisseria meningitidis*
A:Variety: strain C1938
C:Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 20-Jun-2000
C:Accession: S08514
R:Stern, A.; Meyer, T.F.
Mol. Microbiol. 1, 5-12, 1987
A:Title: Common mechanism controlling phase and antigenic variation in pathogenic *neisseria*
A:Reference number: S08513; MUID:88260884
A:Accession: S08514
A:Molecule type: DNA
A:Residues: 1-258 <STE>
A:Cross-references: EMBL:X06445; NID:g44906; PID:g1333787
A:Experimental source: strain C1938
A:Note: expression of opacity proteins is regulated by the number of translated repeat e
of repeats. Place the start codon in frame with the rest of the protein
C:Genetics:
A:Gene: Opm1

```

C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-13,14-Domain: signal sequence (fragments) #status predicted <SIG>
F:22-258/Produce: opacity protein-related protein OPM1 #status predicted <NMT>
F:33-41/Domain: transmembrane #status predicted <TM1>
F:42-73/Domain: extracellular #status predicted <EXT1>
F:50-59/Region: semivariable region
F:74-82/Domain: transmembrane #status predicted <TM2>
F:87-93/Domain: transmembrane #status predicted <TM3>
F:94-129/Domain: extracellular #status predicted <EXT2>
F:100-124/Region: hypervariable region HV1
F:130-144/Domain: transmembrane #status predicted <TM4>
F:150-160/Domain: transmembrane #status predicted <TM5>
F:161-209/Domain: extracellular #status predicted <EXT3>
F:166-215/Region: hypervariable region HV2
F:210-222/Domain: transmembrane #status predicted <TM6>
F:226-234/Domain: transmembrane #status predicted <TM7>
F:235-249/Domain: extracellular #status predicted <EXT4>
F:250-258/Domain: transmembrane #status predicted <TM8>

Query Match      27.4%      Score 238: DB 2; Length 258;
Best Local Similarity 28.5%      Pred. No. 4,9e-14;
Matches 70; Conservative 29; Mismatches 67; Indels 80; Gaps 7;

```

RESULT 12

S20043
opacity protein B precursor (clone pFIOB1700) - *Neisseria meningitidis* (strain FAM18) (th

N:Alternate names: outer membrane protein class 5
C:Species: *Neisseria meningitidis*
A:Variety: strain FAM18
C:Date: 04-Jun-1997 #sequence_revision 04-Jun-1997 #text_change 17-Oct-1997
C:Accession: S20043
R:Alho, E.L.; Dempsey, J.A.; Hobbs, M.M.; Klapper, D.G.; Cannon, J.G.
Mol. Microbiol. 5, 1429-1437, 1991
A>Title: Characterization of the opa (class 5) gene family of *Neisseria meningitidis*.
A:Reference number: S16286; MUID: 92157869
A:Accession: S20043
A:Molecule type: DNA
A:Residues: 1-254 <AHO>
A:Cross-references: EMBL:X63108
A:Experimental source: strain FAM18; clone pFLO1700
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
A:Note: only a part of the translation is shown
A:Note: expression of opacity proteins is regulated by the number of translated repeats of repeats place the start codon in frame with the rest of the protein
C:Genetics:

Query Match	Score 23%	DB 2:	Length 254:
Best Local Similarity	28.3%	Pred. No. 5,9e-14:	
Matches 69; Conservative	31;	Mismatches 66;	Indels 78; Gaps 7.

RESULT 13

S04380
opacity protein P.II precursor - Neisseria gonorrhoeae (strain F62-SF and others) (F62-SF)
C:Species: Neisseria gonorrhoeae
A:Variety: strain F62-SF
C:Date: 30-Jun-1991 #sequence_revision 17-Oct-1997 #text_change 13-Nov-1998
C:Accession: S04380; S16504
R:Palmer, L.; Brooks, G.F.; Falkow, S.

Mol. Microbiol. 3, 663-671, 1988
 A:Title: Expression of gonococcal protein II in *Escherichia coli* by translational fusion
 A:Reference number: S04380; MUID:89343653
 A:Accession: S04380
 A:Molecule type: DNA
 A:Residues: 1-270 <PAL>
 A:Cross-references: EMBL:X15780
 A:Experimental source: strain F62-SF, serogroup IB-3; clone F62-SFG1
 A:Note: the authors did not translate the sequence of the signal peptide
 A:Note: expression of opacity proteins is regulated by the number of translated repeat
 of repeats place the start codon in frame with the rest of the protein
 R:Tab, M.K.; So, M.; Selfert, H.S.; Bilyard, E.; Marchal, C.
 EMBL J. 7, 4367-4378, 1988
 A:Title: Pilin expression in *Neisseria gonorrhoeae* is under both positive and negative
 A:Reference number: S02017; MUID:89210824
 A:Accession: S16504
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 259-270 <TAH>
 A:Cross-references: EMBL:X19665
 A:Experimental source: strain MS11A
 A:Note: expression of opacity proteins is regulated by the number of translated repeat
 of repeats place the start codon in frame with the rest of the protein
 C:Genetics:
 A:Gene: opa1
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-270/Product: opacity protein opa #status predicted <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-75/Domain: extracellular #status predicted <EXT1>
 F:51-61/Region: semivariable region
 F:76-84/Domain: transmembrane #status predicted <TM2>
 F:89-95/Domain: transmembrane #status predicted <TM3>
 F:96-141/Domain: extracellular #status predicted <EXT2>
 F:102-136/Region: hypervariable region HV1
 F:142-156/Domain: transmembrane #status predicted <TM4>
 F:162-172/Domain: transmembrane #status predicted <TM5>
 F:173-221/Domain: extracellular #status predicted <EXT3>
 F:178-227/Region: hypervariable region HV2
 F:228-234/Domain: transmembrane #status predicted <TM6>
 F:238-246/Domain: transmembrane #status predicted <EXT4>
 F:247-261/Domain: extracellular #status predicted <EXT5>
 F:262-270/Domain: transmembrane #status predicted <TM6>
 Query Match 27.3%; Score 237; DB 2; Length 270;
 Best Local Similarity 27.1%; Pred. No. 6.3e-14;
 Matches 72; Conservative 33; Mismatches 67; Indels 94; Gaps 8;

OY 2 KKALATLIALPAAALAE---ASGTYVQADAH-----AKASSLSGSAK 44
 DB 6 KKPSSILFSSLSMAQAAGGNGRPPYQADLAAYEHITHDYPKPTGAKKGTTSIVS 65
 OY 45 GF-----SPRISAGYRINDLRFANDYTRYK----- 69
 DB 66 DYFNRIHTSHVPRSVSYDGCGRRIADYARKMNNKTSVSIKELGRNDSASGVRG 125
 OY 70 --NKAPSTDR-----LYSIGASALYDDTOSPVKPYLGARLSL----- 107
 DB 126 HLNIDTQTEHQENGTFHAASLSLSTIYDDTOSRFRPYIGAVAGVHRHGYRVEOE 185
 OY 108 -----NRASVYDGS-----DSFQSTSLGLVLTGVSAVTPNVLDLGGYR 148
 DB 186 TEIVTTTKEQNVASPPGAPYKPPAHNHSRSLSLGFGAVAGVIDITPNTLDAGYR 245
 OY 149 YNYIGKVTYKRVSGELSGVGRVKE 174
 DB 246 YHNGRLENTN-R-FKTHASLSGVRVRF 270

RESULT 14
 KONTZC
 opacity protein P.IIC precursor - *Neisseria gonorrhoeae* (strain J53) (fragments)

N:Alternate names: outer membrane protein P.IIC
 C:Species: *Neisseria gonorrhoeae*
 A:Variety: strain J53
 C:Date: 31-Mar-1992 #sequence_revision 17-Oct-1997 #text_change 08-May-1998
 C:Accession: S03095; S16360
 R:van der Ley, P.
 Mol. Microbiol. 2, 797-806, 1988
 A:Title: Three copies of a single protein II-encoding sequence in the genome of *Neiss*
 A:Reference number: S03095; MUID:89096501
 A:Accession: S03095
 A:Molecule type: DNA
 A:Residues: 1-268 <VAN>
 A:Cross-references: EMBL:X12625
 A:Experimental source: strain J53
 A:Note: 241-Val was also found
 A:Note: expression of opacity proteins is regulated by the number of translated repea
 of repeats place the start codon in frame with the rest of the protein
 R:Barltt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
 Infect. Immun. 55, 2026-2031, 1987
 A:Title: Antigenic and structural differences among six proteins II expressed by a sl
 A:Reference number: S16360; MUID:87306843
 A:Accession: S16360
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 24-34 <BAR>
 C:Genetics:
 A:Gene: pilC
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-268/Product: opacity protein P.IIC #status experimental <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-74/Domain: extracellular #status predicted <EXT1>
 F:51-60/Region: semivariable region
 F:75-83/Domain: transmembrane #status predicted <TM2>
 F:88-94/Domain: transmembrane #status predicted <TM3>
 F:95-140/Domain: extracellular #status predicted <EXT2>
 F:101-135/Region: hypervariable region HV1
 F:141-155/Domain: transmembrane #status predicted <TM4>
 F:161-171/Domain: transmembrane #status predicted <TM5>
 F:172-219/Domain: extracellular #status predicted <EXT3>
 F:177-225/Region: hypervariable region HV2
 F:220-232/Domain: transmembrane #status predicted <TM6>
 F:236-244/Domain: transmembrane #status predicted <TM7>
 F:245-259/Domain: extracellular #status predicted <EXT4>
 F:260-268/Domain: transmembrane #status predicted <TM8>
 Query Match 27.2%; Score 236.5; DB 1; Length 268;
 Best Local Similarity 26.8%; Pred. No. 7e-14;
 Matches 69; Conservative 32; Mismatches 67; Indels 89; Gaps 8;

OY 6 ATLIALALPAAALAEASGTYVQADAAHAKA-----SSLSGSAK----- 44
 DB 13 SLLFSSMAAASSEDGCRGTYVQADLAAYEHITHDYPKPTGKNNKISTVSDFRINT 72
 OY 45 -GSPRISAGYRINDLRFANDYTRYK-----NYKAPS 75
 DB 73 HSHVPRSVSYDGCGRRIADYARKMNNKTSVSIKELGRNDSASGVGRHNLNQYK 132
 OY 76 TDRK-----LYSIGASALYDDTOSPVKPYLGARLSLNR-----SYDL----- 114
 DB 133 TEHQENGTFHAASLSLSTIYDDTOSRFRPYIGMRYAVAGVHRHGYRVEOEETETITTP 192
 OY 115 ---GSDPSFSQ-----TSIGLGYLTGVSAVTPNVLDLGGYRNYNYGKVT 157
 DB 193 SNGGKGVSLSSKMPKPSAHNHSIRRVGLVAGVGFITPNTLDGTYRHNGRLEN 252
 OY 158 VKNVRSGELSGVGRVKE 174
 DB 253 TR-FKTHASLSGVRVRF 268

RESULT 15

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:55:44 ; Search time 6.98996 Seconds

(without alignments)
963.840 Million cell updates/sec

Title: US-09-684-883-2

Perfect score: 866
Sequence: 1 MKKALATLIALPALPAALAE.....VNTVKNVSGELSYGVKVF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	240.5	27.7	237 1	OPAK_NEIGO
2	239	27.5	260 1	OPRL_NEIMC
3	236.5	27.2	270 1	OPMC_NEIGO
4	235	27.1	236 1	OPAC_NEIGO
5	232.5	26.8	234 1	OPAD_NEIGO
6	232.5	26.8	237 1	OPAB_NEIGO
7	232	26.7	234 1	OPAE_NEIGO
8	232	26.7	234 1	OPAF_NEIGO
9	231	26.6	233 1	OP67_NEIGO
10	226	26.0	234 1	OP28_NEIGO
11	226	26.0	234 1	OP65_NEIGO
12	226	26.0	238 1	OP66_NEIGO
13	226	26.0	238 1	OPAH_NEIGO
14	224.5	25.9	243 1	OPAD_NEIGO
15	224	25.8	244 1	OPAL_NEIGO
16	219	25.2	238 1	OP68_NEIGO
17	217	25.0	178 1	YE57_HAEIN
18	215	24.8	239 1	OPAA_NEIGO
19	205.5	23.7	247 1	OPAG_NEIGO
20	180	20.7	121 1	OPA_HAEIN
21	135	15.6	170 1	OPR3_NEIMC
22	126.5	14.6	70 1	Y414_HAEIN
23	108	12.4	182 1	AIL_YERPS
24	100	11.5	213 1	OM25_BRUVB
25	98.5	11.3	350 1	OMPA_SATRY
26	97.5	11.2	341 1	OMPU_VIBCH
27	94.5	10.9	212 1	OMFW_ECOLI
28	94	10.8	349 1	OMPA_BUCOL
29	94	10.8	353 1	OM51_HAEIN
30	93	10.7	521 1	TSAS_RICIS
31	92	10.6	213 1	OM25_BRUSD
32	90.5	10.4	428 1	OM47_PASND
33	90	10.4	213 1	OM25_BRUME

34	90	10.4	353 1	OM52_HAEIN	P38368 haemophilus
35	89	10.3	178 1	AIL_YEREN	P16454 yersinia en
36	88.5	10.2	346 1	OMPA_ECOLI	P02934 escherichia
37	88	10.1	359 1	OM53_HAEIN	P45996 haemophilus
38	86	9.9	201 1	OM25_BRUVB	P45335 brucella ov
39	86	9.9	213 1	OM25_BRUCA	P45110 brucella ca
40	84.5	9.7	350 1	OMPA_ENTAE	P09146 enterobacte
41	84.5	9.7	995 1	Y109_YEAST	P40442 saccharomyc
42	84	9.7	213 1	OM25_BRUNE	P45326 brucella ne
43	84	9.7	350 1	PORF_PSEAE	P13794 pseudomonas
44	82.5	9.5	350 1	PHOE_ENTCL	P47490 enterobacte
45	82	9.4	433 1	FTSZ_ARATH	P42545 arabidopsis

ALIGNMENTS

RESULT 1	OPAK_NEIGO	STANDARD	PRT	237 AA.
ID	OPAK_NEIGO			
AC	Q04880			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	01-NOV-1995 (Rel. 32, Last annotation update)			
DE	Opacity Protein OPA57 precursor (Fragment).			
GN	OPAK.			
OS	Neisseria gonorrhoeae.			
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=485;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MS11 / F3;			
RA	MEDLINE=93178439; PubMed=8440254;			
RT	Kusch E.-M., Kueper B., Kuroki T., Heuer I., Meyer T.F.;			
RT	"Variable opacity (Opa) outer membrane proteins account for the cell			
RT	tropisms displayed by Neisseria gonorrhoeae for human leukocytes and			
RT	epithelial cells."			
RL	EMBO J. 12:641-650(1993).			
CC	-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA			
CC	PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE			
CC	VARIATION.			
CC	-1- SUBCELLULAR LOCATION: Outer membrane.			
CC	-----			
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CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL: Z18935; CAA79368.1; -			
DR	PIR: S28626; S28626.			
DR	InterPro: IPR003394; Opacity.			
DR	Pfam: PF02462; Opacity; 1.			
KW	Outer membrane; Multigene family; signal.			
FT	NON_TER	1		
FT	SIGNAL	<1	1	POTENTIAL.
FT	CHAIN	2	>237	OPACITY PROTEIN OPA57.
FT	NON_TER	237		
SO	SEQUENCE	237 AA; 26703 MW; F8B1A0B5C7BECAD CRC64;		
Query Match	27.7%; Score 240.5; DB 1; Length 237;			
Best Local Similarity	29.6%; Pred. No. 4.4e-15;			
Matches	71; Conservative 26; Mismatches 58; Indels 85; Gaps 9;			
OY	17 ALAAGAGFYQADAAHA-----KASSLSG-----ANGFSRISAGY 54			
DB	1 ASEGGGRPYQADLAAYEHIHIDYEPAPNKNKISTVSDYRNITRISVHPVSVG 60			
OY	55 RINDRFADVDTTRYKNY-----KASTDFK-----LXSGAS 86			
DB	61 DFGGRRIADYARFKRMNNKYSVSIKELLRNKNGNMTDKLENQNGTFHAYVSLG 120			


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QY 87 AAYDFDQSPVYKPYLGARLSLN--RASVD-----LGS-----116
|:|:| |:|:|:|:|:| |:|:|
DB 121 AAYDFDQSPVYKPYLGARLSLN--RASVD-----LGS-----116
|:|:| |:|:|:|:|:| |:|:|
QY 117 --SDSFQTSIGLGLVGYSAVTPNDLDAGRYNYTKVNRSGELSGVGRVKE 174
|:|:| |:|:|:|:|:| |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 181 RESDSIR--VGLGAVAGVGIDITPNLTLADGARYHYWGRLENTR-PKTHEASLGVRVRF 237
|:|:| |:|:|:|:|:| |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 2
OPRL_NEIMC STANDARD; PRT; 260 AA.
ID OPRL_NEIMC
AC P10170;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Opacity-related protein POPML.
GN OPR.
OS Neisseria meningitidis (serogroup C).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=135720;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1938 / SEROGROUP C;
RX MEDLINE=8826084; PubMed=2455211;
RA Stern A., Meyer T.F.;
RT "Common mechanism controlling phase and antigenic variation in
pathogenic neisseriae."
RL Mol. Microbiol. 1:5-12(1987).
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -1- SIMILARITY: STRONG TO THE OPACITY-RELATED PROTEIN POPM3 AND
REGIONS OF HOMOLOG WITH N.GONORRHOEA (STRAIN MS11) OPA GENE
PRODUCTS.
CC -----
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CC -----
DR EMBL, X06445; CA29748.1; ALT-SEQ.
DR PIR: S08514; S08514.
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity; 1.
KW Outer membrane.
SQ SEQUENCE 260 AA; 28936 MW; EB47A2843B3F037B CRC64;

Query Match 27.5%; Score 239; DB 1; Length 260;
Best Local Similarity 27.6%; Pred. No. 6.8e-15;
Matches 71; Conservative 34; Mismatches 66; Indels 86; Gaps 8;

```

```

RESULT 3
OMPC_NEIGO STANDARD; PRT; 270 AA.
ID OMPC_NEIGO
AC P09888;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Outer membrane protein P.IIC precursor (Protein IIC).
GN P.IIC.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J53;
RX MEDLINE=89096501; PubMed=3145386;
RA van der Ley P.;
RT "Three copies of a single protein II-encoding sequence in the genome
of Neisseria gonorrhoeae J53: evidence for gene conversion and gene
duplication."
RL Mol. Microbiol. 2:797-806(1988).
CC -1- FUNCTION: THIS PROTEIN SERVES AS A PORIN.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -----
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CC -----
DR EMBL, X12625; CA31144.1; -.
DR PIR: S03095; KONH2C.
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity; 1.
KW Outer membrane; Porin; Transmembrane; Antigen; Signal.
FT SIGNAL 1 25
FT CHAIN 26 270
FT TRANSMEM 36 44 OUTER MEMBRANE PROTEIN P. IIC.
FT TRANSMEM 77 85
FT TRANSMEM 90 96 POTENTIAL.
FT TRANSMEM 143 157 POTENTIAL.
FT TRANSMEM 163 173 POTENTIAL.
FT TRANSMEM 222 234 POTENTIAL.
FT TRANSMEM 228 246 POTENTIAL.
FT TRANSMEM 262 270 POTENTIAL.
SQ SEQUENCE 270 AA; 30269 MW; FB448373830A50D CRC64;

Query Match 27.2%; Score 236.5; DB 1; Length 270;
Best Local Similarity 26.8%; Pred. No. 1.2e-14;
Matches 69; Conservative 32; Mismatches 67; Indels 89; Gaps 8;

```


DB 255 TR-FTHESLGMRYRF 270

RESULT 4

OPAC_NEIGO STANDARD; PRT; 236 AA.

AC P11296;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Opacity protein OPA50 precursor (OPA50) (VO) (Fragment).

GN OPAC.

OS Neisseria gonorrhoeae.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=485;

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN-MS11 / V0;

RX MEDLINE=87002493; PubMed=3093085;

RA Stern A., Brown M., Nickel P., Meyer T.F.;

RT "Opacity genes in Neisseria gonorrhoeae: control of phase and antigenic variation."

RL Cell 47:61-71(1986).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-MS11 / F3;

RX MEDLINE=93178439; PubMed=8440254;

RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

RT "Variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells."

RL EMO J. 12:641-650(1993).

CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE VARIATION.

CC -1- SUBCELLULAR LOCATION: Outer membrane.

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CC EMBL: M14746; NOT_ANNOTATED_CDS.

DR EMBL: Z18927; CAA79360.1; -.

DR PIR: A24428; KONHO.

DR PIR: S28621; S28621.

DR PIR: S36328; S36328.

DR InterPro: IPR003394; Opacity.

DR Pfam: PF02462; Opacity; 1.

KW Outer membrane; Multigene family; Signal.

FT SIGNAL 1 1

FT NON_TER 1 1

FT CHAIN 2 >236 POTENTIAL.

FT NON_TER 236 OPACITY PROTEIN OPA50.

FT SEQUENCE 236 AA; 26685 MW; 68DC237692183398 CRC64;

Query Match 27.1%; Score 235; DB 1; Length 236;

Best Local Similarity 29.3%; Pred. No. 1,4e-14;

Matches 70; Conservative 26; Mismatches 59; Indels 84; Gaps 9;

DB 17 ALAAGAGGYVADAAHA-----KASSSLGSAKGF-----PRISAGY 54

DB 1 ASDSGRGYVADALAYAEHTHDYPRKPTDSKAKISTVSDYFENIRTHSHPRVSAY 60

DB 55 RINDLFAVDYTRY-----KNYAPSTD-----FKLVSIGAS 86

DB 61 DFGGRIADYARYRRKWDNKKYSVSIKNRVRHKHNSRNKLTENQENGFHAYSSIGLS 120

DB 87 AIDVFTQSGYVRYKYLGRSLN--RASVD-----LGG----- 116

DB 121 AIDVFOINDKFKYIGARVAGVHRHSIDSTFKKITGLTTSPGINSGYKYLRTPGAHR 180

DB 117 -SDSFQTSIGLVLYGVAATPVNDLADGARYNYTKGVNKNVRSGLSVGRVKE 174

DB 181 ESDSIR--VGLGYIAGVGFDITPKLTLDDGCRYRHHNWRLENTN--FKTHASLGVRYRF 236

RESULT 5

OPAR_NEIGO STANDARD; PRT; 234 AA.

ID OPAR_NEIGO

AC 004874;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Opacity protein OPA51 precursor (Fragment).

GN OPAR.

OS Neisseria gonorrhoeae.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=485;

RP SEQUENCE FROM N.A.

RC STRAIN-MS11 / F3;

RX MEDLINE=93178439; PubMed=8440254;

RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

RT "Variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells."

RL EMO J. 12:641-650(1993).

CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE VARIATION.

CC -1- SUBCELLULAR LOCATION: Outer membrane.

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CC EMBL: Z18928; CAA79361.1; -.

DR PIR: S28628; S28628.

DR PIR: S36329; S36329.

DR InterPro: IPR003394; Opacity.

DR Pfam: PF02462; Opacity; 1.

KW Outer membrane; Multigene family; Signal.

FT SIGNAL 1 1

FT NON_TER 1 1

FT CHAIN 2 >234 POTENTIAL.

FT NON_TER 234 OPACITY PROTEIN OPA51.

FT SEQUENCE 234 AA; 26772 MW; 9FEB5B5DABBA96CA CRC64;

Query Match 26.8%; Score 232.5; DB 1; Length 234;

Best Local Similarity 29.3%; Pred. No. 2,4e-14;

Matches 69; Conservative 25; Mismatches 61; Indels 79; Gaps 9;

DB 19 AEG-ASGPPYVADAAHA-----KASSSLGSAK-----GFSPRISAGY 55

DB 2 SEGNGRGYVADALAYAEHTHDYPRKPTDSKAKISTVSDYFENIRTHSHPRVSAY 61

DB 56 INDLFAVDYTRY--NYKAPSTD-----LYSIGASAY 89

DB 62 FGGRIADYARYRRKWDNKKYSVDIKELNKNQKRLDKTENQENGFHAYSSIGLSAY 121

DB 90 DEDDQSPKPYLGRSLN--RASVD-----LGG-----SDSF 120

DB 122 DFKLNGKRPYIGARVAGVHRHSIDSTFKKITGLTTSSYGGLNFTYTEONTAHRQSN 181

DB 121 SOTSIGLVLYGVAATPVNDLADGARYNYTKGVNKNVRSGLSVGRVKE 174

DB 182 SIRRGVGLVAGVGFDITPKLTLDDGCRYRHHNWRLENTN--FKTHASLGVRYRF 234

RESULT 6
OPAE_NEIGO
ID OPAE_NEIGO STANDARD; PRT; 237 AA.
AC 004879;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA58 precursor (Fragment).
GN OPAE.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=485;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
epithelial cells."
RT EMO J. 12:641-650(1993).
RL EMO J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
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CC
CC EMBL: Z18937; CAA79370.1; -
CC PIR: S28624; S28624.
CC InterPro: IPR003394; Opacity.
CC Pfam: PF02462; Opacity; 1.
CC Outer membrane; Multigene family; Signal.
CC
CC FT SIGNAL 1 1
CC NON_TER 1 1
CC CHAIN 2 237 POTENTIAL.
CC FT 2 237 OPACITY PROTEIN OPA58.
CC NON_TER 237 237
CC SEQUENCE 237 AA; 26855 MW; B165033B2C8D6A53 CRC64;
Query Match 26.8%; Score 232.5; DB 1; Length 237;
Best Local Similarity 29.6%; Pred. No. 2.4e-14;
Matches 69; Conservative 25; Mismatches 54; Indels 85; Gaps 9;
QY 24 GGYVQADAAHA-----KASSSLGSAKGF-----PRISAGYRINDLR 61
DB 8 GGYVQADAAHAHEITHDPEQTPDSKGIKISTVSDYFRNIRTHSHPRVSGVDFGGMRI 67
QY 62 AVDYTRKRY-----KAPSTDFK-----LYSGASAIYDFDT 93
DB 68 AADYARARKNNNNKYSVSIKELLRKNCNRTRCTENQNGTFHVAVSSLGSAVYDFDKI 127
QY 94 OSPYKPYLGARLSLN--RASVD-----LGG-----SDSR 121
DB 128 NDKFKPYIGARVAAGVHSHSIDSTKTKTEVTTLHGCGTTPVYPEKKNODAHRESDSIR 187
QY 122 QTSIGLGLVGSAAVTPNDLAGRYNYIGKVTNYKVRSGELSGVYKVF 174
DB 188 R--VGLGAVAGVGIDITPRLTDGIRYHMGRLNTR-FKTHASLGYRYRF 237
RESULT 7
OPAE_NEIGO
ID OPAE_NEIGO STANDARD; PRT; 234 AA.
AC 004878;
DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA55 precursor (Fragment).
GN OPAE.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=485;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
epithelial cells."
RT EMO J. 12:641-650(1993).
RL EMO J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC
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CC
CC EMBL: Z18933; CAA79366.1; -
CC PIR: S28632; S28632.
CC InterPro: IPR003394; Opacity.
CC Pfam: PF02462; Opacity; 1.
CC Outer membrane; Multigene family; Signal.
CC
CC FT SIGNAL 1 1
CC NON_TER 1 1
CC CHAIN 2 234 POTENTIAL.
CC FT 2 234 OPACITY PROTEIN OPA55.
CC NON_TER 234 234
CC SEQUENCE 234 AA; 26881 MW; 8EBB30B3A774C766 CRC64;
Query Match 26.7%; Score 232; DB 1; Length 234;
Best Local Similarity 29.4%; Pred. No. 2.6e-14;
Matches 67; Conservative 24; Mismatches 59; Indels 78; Gaps 8;
QY 24 GGYVQADAAHA-----KASSSLGSAK-----GPSRISAGYRINDLR 61
DB 8 GGYVQADAAHAHEITHDPEQTPDKKDKISTVSDYFRNIRTHSHPRVSGVDFGGMRI 67
QY 62 AVDYTRK--NRYKAPSTDFK-----LYSGASAIYDFDTOS 95
DB 68 AADYARARKNNNNKYSVDIKELRNKRDCLKTENQNGTFHVAVSSLGSAVYDFDKND 127
QY 96 PYKPYLGARLSLN--RASVD-----LGG-----SDSRQTSIG 126
DB 128 KFKPYIGARVAAGVHSHSIDSTKTKTKFELTSSGGLNPTVYENTONAHQHSNIRRVG 187
QY 127 LGLTVGSAAVTPNDLAGRYNYIGKVTNYKVRSGELSGVYKVF 174
DB 188 LGVIAGVGEDITPKLTDGIRYHMGRLNTR-FKTHASLGYRYRF 234
RESULT 8
OPAE_NEIGO
ID OPAE_NEIGO STANDARD; PRT; 234 AA.
AC 004879;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA56 precursor (Fragment).
GN OPAE.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=485;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MS11 / F3; PubMed=8440254;
RX MEDLINE=93178439; PubMed=8440254;
RA Kuepich E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
epithelial cells."
RL EMBL J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
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CC -----
DR EMBL: 218934; CAA79367.1; -.
DR PIR: S28620; S28620.
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity.1.
KW Outer membrane; Multigene family; signal.
FT SIGNAL 1 1
FT NON_TER 1 1
FT CHAIN 2 >234 POTENTIAL.
FT NON_TER 234 234 OPACITY PROTEIN OPA56.
SQ SEQUENCE 234 AA; 26868 MW; 5175C606839EFFB CRC64;

Query Match
Best Local Similarity 26.7%; Score 232; DB 1; Length 234;
Matches 66; Conservative 25; Mismatches 59; Indels 78; Gaps 8;

QY 24 GYVQADAAHA-----KASSLSGSAK-----GPSRISAGYRINDLR 61
DB 8 GYVQADLAAYAEHTHDYPEQTKKDKISTVDFRNVRTHSHPRVSVGDEGWR 67
QY 62 ANDYRKYKYPKAP--STDPK-----LYSGASAIYPTQOS 95
DB 68 AADYATYKRWNDKYSVDIKLENNQNKRDIKTENQNGTFHAASLSIGSAVYDFK 127
QY 96 PVKPYLGARLSLN--RASVD-----LGG-----SDSPFSQTSIG 126
DB 128 KFKPYIGAVAYAGVHRHSDSTKTKTKELTSSYGLNPTVYTEENTQNAHHQSNIRAVG 187
QY 127 LGVINGVSAVTPNVDLAGYRYNYIGKYNVKNVRSGLSVGRVKF 174
DB 188 LGVINGVGFDPITPKLTDGYRYHYWGRLENTR-FKTHEASLGAVYRF 234

RESULT 9
OP67_NEIGO
AC Q05034; STANDARD; PRT; 233 AA.
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA67 precursor (Fragment).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VPI;
RA MEDLINE=93178439; PubMed=8440254;
RX Kuepich E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
epithelial cells."

```

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RL EMBL J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
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CC -----
DR EMBL: 218942; CAA79375.1; -.
DR PIR: S28625; S28625.
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity.1.
KW Outer membrane; Multigene family; signal.
FT SIGNAL 1 1
FT NON_TER 1 1
FT CHAIN 2 >233 POTENTIAL.
FT NON_TER 233 233 OPACITY PROTEIN OPA67.
SQ SEQUENCE 233 AA; 26039 MW; 6C13A46A163C67F CRC64;

Query Match
Best Local Similarity 26.6%; Score 231; DB 1; Length 233;
Matches 64; Conservative 31; Mismatches 60; Indels 78; Gaps 7;

QY 19 AEG-ASGYVQADAAHA-----KASSLSGSAKGF-----SPRISAGY 54
DB 2 SEGNGRGPYVQADLAAYAEHTHDYPEATQAKKGTITSTVDFRNIRTHSVPRVSVG 61
QY 55 RINDLRFAVDTYRKNT-----KASTDEKLSIGASAIYDD 92
DB 62 DFGGWRITADYARARKNNNSKYSYIKKIONOYKKTENQNGTFHAASLSIGSAVYDFK 121
QY 93 TQSPVKPYLGARLSLN--RASVDL-----GSDSPS 121
DB 122 LNDKFKPYIGARVAYAGVHRHSDSTKTKTGFLTTAGARGAAPVSSPYKQTQDAHDESN 181
QY 122 QTSIGLGVLSAVTPNVDLAGYRYNYIGKYNVKNVRSGLSVGRVKF 174
DB 182 IRRVGLGVINGVGFDPITPKLTDGYRYHNMGRLENTR-FKTHEASLGAVYRF 233

RESULT 10
OP28_NEIGO
AC P11297; STANDARD; PRT; 234 AA.
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Opacity protein V28 precursor (Fragment).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=87002493; PubMed=3093085;
RX Stern A., Brown M., Nickel P., Meyer T.F.;
RT "Opacity genes in Neisseria gonorrhoeae: control of phase and
antigenic variation."
RL Cell 47:61-71(1986).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M14747; -; NOT_ANNOTATED_CDS.
DR PIR; B24429; KONH8.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity: 1.
KW Outer membrane; Multigene family; Signal.
FT NON_TER 1
FT SIGNAL <1 1 POTENTIAL.
FT CHAIN 2 >234 OPACITY PROTEIN V28.
FT NON_TER 234 234
SQ SEQUENCE 234 AA; 26770 MW; 339AE80962FE75E4 CRC64;

Query Match 26.0%; Score 226; DB 1; Length 234;
Best Local Similarity 29.4%; Pred. No. 9.3e-14;
Matches 67; Conservative 24; Mismatches 59; Indels 78; Gaps 8;

OY 24 GRYVQADAAHA-----KASSSLGSASAK-----GSPRISAGYRINDLRF 61
DB 8 GRVYQADLAAYAEHITHDYPEPTGFKKDKISTVSDYFNIRFTHSHPRVSGYDGGWRI 67
OY 62 AVDYTRYK--NYKAPSTDFK-----LYSGASATYFDIOS 95
DB 68 RADYARYRKMNDNKKYSVICKELNNQNRDKLTENQENGPFHAVSSIGLSAVDFKLN 127
OY 96 PVKPYIGARLSIN--RASVD-----LGG-----SDSFQTSIG 126
DB 128 KKPFIIGARVAAGHRRHSIDSTKTKTKFLTSSYGLINPTVYEENTQNAHNSIRKVG 187
OY 127 LGLVLTGSAVTAVPNVDLAGRYRNTIGKVNIVKNSGELSYGVKVF 174
DB 188 LGVINGVGFDIPKLTLDAGRYRHMGGRLENNR-FKTHRASLSGVRYRF 234

RESULT 11
OP65_NEIGO
OP65_NEIGO STANDARD; PRT; 234 AA.
AC 004885;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OP65 precursor (Fragment).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI;
RX MEDLINE=931178439; PubMed=8440254;
RA Kupsch E.-M., Knupper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells.";
RL EMO J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC
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CC
DR EMBL; Z18940; CAI79373.1; -.
DR PIR; S28617; S28617.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.

```

```

KW Outer membrane; Multigene family;Signal.
FT NON_TER 1 1 POTENTIAL.
FT SIGNAL <1 1 OPACITY PROTEIN OPA65.
FT CHAIN 2 >234
FT NON_TER 234 234
SQ SEQUENCE 234 AA; 26242 MW; D66A0BA8A424C2P1 CRC64;

Query Match 26.0%; Score 226; DB 1; Length 234;
Matches 64; Conservative 28.1%; Pred. No. 9,3e-14; Mismatches 58; Indels 78; Gaps 8;

QY 24 GFYYGADAHA-----KASSSIGS-----AKGFSPRISAGRYINDLRF 61
   | | | | | : | | | | | | | | | | | | | | | | | | | | | |
DB 8 GPYYOADIATYAERTIDHPETPGAKKAOLSTVSDFNIRITHSIHPSVYGDFGWRI 67
   |||::|||::| | | | | | | | | | | | | | | | | | | | | |
QY 62 ANDYRRYK-----NKRASTDCK-----LYTIGASALTYPDROSP 96
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 68 ADADYRKRWKESNSIKKVEDIKDKTKETEKGNGCTFHAVSSLSLSTIYDQISDK 127
   |||::|||::| | | | | | | | | | | | | | | | | | | | | |
QY 97 VKPYLGARL-----SLNRASVDL-----GG-----SDSEFSQTSIG 126
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 128 IKPIGVHRVGCHVAHQYRSVQGQETITVTLPKPKNGTOGGPVKSTSPIDAYHENRSSRLG 187
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 127 LCVLTGSVSYATVPNDLDAGRYRNATIGVNYKYKRSGELSVGYVKF 174
   - - - - - | - - - - - | | | | | | | | | | | | | | | | |
DB 188 FGAMAGVIDVAPGLTLDAGRYHYHWGLENTFR-EKTDEASLGVRYRF 234

RESULT 12
OP66_NEIGO
ID OP66_NEIGO STANDARD: PRI: 238 AA.
AC 005033:
DC 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DI 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA66 precursor (Fragment).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VPL;
RX MEDLINE=931178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuraki T., Heuer I., Meyer T.F.;
RT "Variable opacity (opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells.";
RL EMBO J. 12:641-650(1993).
CC -! FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -! SUBCELLULAR LOCATION: Outer membrane.
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CC -----
DR EMBL, Z18941; CAA79374.1; -.
DR PIR, S28619; S28619.
DR InterPro: IPR003394; Opacity.
DR Pfam, PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.
FT SIGNAL 1 1 POTENTIAL.
FT NON_TER <1 1
FT CHAIN 2 >238 OPACITY PROTEIN OPA66.
FT NON_TER 238 238
SQ SEQUENCE 238 AA; 26888 MW; B6E38AF1585263AA CRC64;

Query Match 26.0%; Score 226; DB 1; Length 238;
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Best Local Similarity 28.4%; Pred. No. 9.5e-14;
Matches 66; Conservative 27; Mismatches 57; Indels 82; Gaps 8;

QY 24 GPVQADAAH-----KASSSLGSAKF-----SPRISAGYRINDLR 61
DB 8 GPVQADAAHAYEHITHDYPRKPTDPSKGLSTVSDYFRNIRTHSHRVSVDGDFGMR 67
QY 62 AVDTTRK--NYKAPSDER-----LYSIGASATYDFDT 93
DB 68 AADTARTRKMDSKYSVSTINLQRTSNGNRDRKTEQNGSFHVAVSSGLSAVDKFL 127
QY 94 QSPVRYLARGRLSLN--RASVD-----LGSD-----SFSQ 122
DB 128 NDKFKPYIGARVAGVHRHSIDSTKTEFLTAGARGTPTVSSPKYQTQDAHESNST 187
QY 123 TSGIGLVTVSAVTPNVLDAGRYRNYIGKVTYKAVNSGELSVGVRYKF 174
DB 188 RRGVLGVLGAVGFDITPNTLDAGRYRNYHNGMLENTR-FKTHASLGVRVRF 238

RESULT 13

OPAD_NEIGO STANDARD; PRT; 238 AA.
AC 004884;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Opacity protein OPA60 precursor (Fragment).
GN OPAH.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_Taxid=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells.";
RL EMBO J. 12:641-650(1993).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / V18;
RX MEDLINE=92114767; PubMed=1815562;
RA Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnig F.,
RT Stern A., Kupsch E.-M., Meyer T.F., Swanson J.;
RT "The opacity proteins of Neisseria gonorrhoeae strain MS11 are
RT encoded by a family of 11 complete genes.";
RL Mol. Microbiol. 5:1889-1901(1991).
RN [3]
RP ERRATUM.
RX MEDLINE=92261323; PubMed=1584024;
RA Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnig F.,
RT Stern S., Kupsch E.-M., Meyer T.F., Swanson J.;
RL Mol. Microbiol. 6:1073-1076(1992).

-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
VARIATION.
-1- SUBCELLULAR LOCATION: Outer membrane.

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CC EMBL; Z18939; CAA79372.1; -;
DR EMBL; X60711; CAA43121.1; -;
DR PIR; S28631; S28631.
DR InterPro; IPR003394; Opacity.

DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.

FT SIGNAL 1 1
FT CHAIN 2 2
FT VARIANTS 2 238
FT VARIANTS 234 234
FT NON_TER 238 238
SQ SEQUENCE 238 AA; 27073 MW; 883A3560C2DF1B9F CRC64;

Query Match 26.0%; Score 226; DB 1; Length 238;
Best Local Similarity 27.6%; Pred. No. 9.5e-14;

Matches 66; Conservative 26; Mismatches 65; Indels 82; Gaps 6;

QY 17 ALAEGSGFYQADAAH-----KASSSLG-----AKSPRISAGY 54
DB 1 AEDDGRGYPVQADAAHAYEHITHDYPPRPAPKNKISTVSDYFRNIRTHSHRVSVDG 60
QY 55 RINDRFAVDYRKYNY-----KAPDFKLYSIGAS 86
DB 61 DGGWRIRADYARVYKRNKNNKYSVNIENVRIKENGITIDRKTEQNGTFHVAVSSGLS 120
QY 87 ATYDFDPSPVKPYLGARSLN--RASVD-----LG 115
DB 121 ATYDFDPSPVKPYLGARVAGVHRHSIDSTKTEFLTAGARGTPTVSSPKYQTQDAHESNST 180
QY 116 GSDSFGTSGIGLVTVSAVTPNVLDAGRYRNYIGKVTYKAVNSGELSVGVRYKF 174
DB 181 DYQNSIRRGVLGVLGAVGFDITPNTLDAGRYRNYHNGMLENTR-FKTHASLGVRVRF 238

RESULT 14

OPAD_NEIGO STANDARD; PRT; 243 AA.
AC 004883;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA59 precursor (Fragment).
GN OPAD.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_Taxid=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells.";
RL EMBO J. 12:641-650(1993).
RN [2]

-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
VARIATION.
-1- SUBCELLULAR LOCATION: Outer membrane.

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CC EMBL; Z18938; CAA79371.1; -;
DR PIR; S28629; S28629.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.
FT SIGNAL 1 1
FT CHAIN 2 243
FT POTENTIAL.
FT OPACITY PROTEIN OPA59.

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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:56:04 ; Search time 19.9713 Seconds
(without alignments)
1507.218 Million cell updates/sec

Title: US-09-684-883-2
Perfect score: 1 MKKALTLRLALPAAALAE.....VNTKRVSGELSGVRKAF 174
Sequence: 868

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhcc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP rivirus:*
16: SP bacteriophage:*
17: SP archaeop:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	174	2 P96943	P96943 neisseria m
2	864	99.5	174	16 Q9RP17	Q9RP17 neisseria m
3	857	98.7	174	2 Q9R2R1	Q9R2R1 neisseria m
4	854	98.4	174	16 P95372	P95372 neisseria m
5	852	98.2	174	2 Q9RP16	Q9RP16 neisseria m
6	846	97.5	174	2 Q9RP18	Q9RP18 neisseria m
7	825	95.0	174	2 P95343	P95343 neisseria g
8	824.5	95.0	175	2 P95371	P95371 neisseria g
9	247	28.5	256	2 051124	051124 neisseria m
10	246.5	28.4	186	16 09CM19	09CM19 pasteurella
11	244	28.1	234	2 Q9R719	Q9R719 neisseria m
12	244	28.1	234	2 007280	007280 neisseria m
13	243	28.0	234	2 Q9R718	Q9R718 neisseria m
14	241.5	27.8	232	2 Q9K4T9	Q9K4T9 neisseria 1
15	241.5	27.8	241	2 Q9AE80	Q9AE80 neisseria 1
16	240.5	27.7	230	2 Q9R9A7	Q9R9A7 neisseria m

17	240	27.6	241	2	Q9K4T4	Q9K4T4 neisseria 1
18	240	27.6	256	2	Q51126	Q51126 neisseria m
19	240	27.6	259	2	Q51125	Q51125 neisseria m
20	239.5	27.6	232	2	Q9R3P5	Q9R3P5 neisseria m
21	238.5	27.5	257	2	Q50929	Q50929 neisseria f
22	238	27.4	234	2	Q07287	Q07287 neisseria m
23	238	27.4	237	2	Q31176	Q31176 neisseria m
24	237	27.3	262	2	Q33388	Q33388 neisseria m
25	236.5	27.2	232	2	Q9K4T3	Q9K4T3 neisseria s
26	236	27.2	270	2	Q9R0V4	Q9R0V4 neisseria m
27	236	27.2	283	2	Q50943	Q50943 neisseria g
28	234.5	27.0	241	2	Q07274	Q07274 neisseria m
29	234	27.0	240	2	Q07925	Q07925 neisseria m
30	234	27.0	272	2	Q51013	Q51013 neisseria g
31	233.5	26.9	241	2	Q07912	Q07912 neisseria m
32	233.5	26.9	253	2	Q51303	Q51303 neisseria s
33	233	26.8	233	2	Q9K4T5	Q9K4T5 neisseria 1
34	233	26.8	235	2	Q30753	Q30753 neisseria 1
35	232.5	26.8	232	2	Q9R9A9	Q9R9A9 neisseria m
36	232.5	26.8	232	2	Q9R9A8	Q9R9A8 neisseria m
37	232	26.7	237	2	Q9K4T6	Q9K4T6 neisseria 1
38	231	26.6	235	2	Q30752	Q30752 neisseria m
39	229.5	26.4	232	2	Q9K4T7	Q9K4T7 neisseria 1
40	228.5	26.3	241	2	Q07273	Q07273 neisseria m
41	228	26.3	242	2	Q9K4T8	Q9K4T8 neisseria 1
42	227.5	26.2	238	2	Q31172	Q31172 neisseria m
43	227.5	26.2	243	2	Q07278	Q07278 neisseria m
44	227	26.2	260	2	Q33389	Q33389 neisseria m
45	226.5	26.1	242	2	Q07279	Q07279 neisseria m

ALIGNMENTS

RESULT 1
P96943 PRELIMINARY; PRT; 174 AA.
AC P96943;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE OUTER MEMBRANE PROTEIN PRECURSOR.
GN NSP.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=608B;
RA MEDLINE=97149429; PubMed=8996237;
RX Martin D., Cadieux N., Hamel J., Brodeur B.R.;
RT "Costimulation of T cell activation by Integrin-associated protein (CD47) is an adhesion-dependent, CD28-independent signaling pathway.";
RL J. Exp. Med. 185:1-11(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NGP165, M986, AND NG6/88;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
DR EMBL; U52066; AAC36000.1; -;
DR EMBL; AF175683; AAD53286.1; -;
DR EMBL; AF175680; AAD53283.1; -;
DR EMBL; AF175682; AAD53285.1; -;
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity; 1.
FT Signal.
FT SIGNAL.
SQ SSOURCE 174 AA; 18425 MW; EBB02767DDCFE19 CRC64;
Query Match 100.0%; Score 868; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.7e-64;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSKGSPRISAGYRINDLR 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDFPKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 FAVDYTRYKNYKAPSTDFPKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
QY 121 SQTSGIGLVLTGVSVAATPVNDLDAGYRNYIGKNTVKNVNSGELSGYRKF 174
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 SQTSGIGLVLTGVSVAATPVNDLDAGYRNYIGKNTVKNVNSGELSGYRKF 174

```

RESULT 2

Q9RP17 PRELIMINARY; PRT; 174 AA.

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AC 09RP17;
DT 01-MAY-2000 (TREMblrel, 13, Created)
DT 01-MAY-2000 (TREMblrel, 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel, 19, Last annotation update)
DE SURFACE PROTEIN A (OUTER MEMBRANE PROTEIN NSGA).
GN NSPA OR NMB0663.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487, 491;
RN 1]
RP SEQUENCE FROM N.A.
RC STRAIN=CU385;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
   among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
RN 12]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=2017575; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Clecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
RA Cotton M.D., Ulterback T.R., Knouri H., Qin H., Vamathevan J.,
RA Gill J., Scariato V., Maignan V., Pizsa M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
   MC58.";
RL Science 287:1809-1815(2000).
DR EMBL; AF175678; AAD53281.1; -.
DR EMBL; AE002420; AAF41081.1; -.
DR TIGR; NMB0663; -.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KW Complete proteome.
SQ SEQUENCE 174 AA; 18397 MW; E8B02767DDC6E109 CRC64;

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Query Match 99.5%; Score 864; DB 16; Length 174;
 Best Local Similarity 99.4%; Pred. No. 5,7e-64;
 Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSKGSPRISAGYRINDLR 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDFPKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 FAVDYTRYKNYKAPSTDFPKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
QY 121 SQTSGIGLVLTGVSVAATPVNDLDAGYRNYIGKNTVKNVNSGELSGYRKF 174
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 SQTSGIGLVLTGVSVAATPVNDLDAGYRNYIGKNTVKNVNSGELSGYRKF 174

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RESULT 3

Q9R2R1 PRELIMINARY; PRT; 174 AA.

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AC 09R2R1;
DT 01-MAY-2000 (TREMblrel, 13, Created)
DT 01-MAY-2000 (TREMblrel, 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel, 17, Last annotation update)
DE SURFACE PROTEIN A.
GN NSPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN 1]
RP SEQUENCE FROM N.A.
RC STRAIN=M136, AND B232;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
   among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
DR EMBL; AF175679; AAD53280.1; -.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
SQ SEQUENCE 174 AA; 18385 MW; ECF6F39A9286910E CRC64;

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Query Match 98.7%; Score 857; DB 2; Length 174;
 Best Local Similarity 98.3%; Pred. No. 2.2e-63;
 Matches 171; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSKGSPRISAGYRINDLR 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDFPKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 FAVDYTRYKNYKAPSTDFPKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
QY 121 SQTSGIGLVLTGVSVAATPVNDLDAGYRNYIGKNTVKNVNSGELSGYRKF 174
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 SQTSGIGLVLTGVSVAATPVNDLDAGYRNYIGKNTVKNVNSGELSGYRKF 174

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RESULT 4

P95372 PRELIMINARY; PRT; 174 AA.

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AC P95372;
DT 01-MAY-1997 (TREMblrel, 03, Created)
DT 01-MAY-1997 (TREMblrel, 03, Last sequence update)
DT 01-DEC-2001 (TREMblrel, 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN PRECURSOR.
GN NSPA OR NMA0862.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487, 65699;
RN 1]
RP SEQUENCE FROM N.A.
RC STRAIN=24063;
RA Martin D., Cadieux N., Hamel J., Rioux C., Brodeur B.R.;
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
RN 12]
RP SEQUENCE FROM N.A.
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltham T., Hamlin N., Holtroyd S.,
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria

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RT meningitidis Z2491."
 RL Nature 404:502-506(2000).
 DR EMBL; U52068; AAB41580.1; -.
 DR EMBL; AL162754; CAB84143.1; -.
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity: 1.
 DR Signal; Complete proteome.
 KW SIGNAL.
 FT SIGNAL.
 SQ SEQUENCE 174 AA; 18355 MW; E8A4A1AD4F6F009 CRC64;

Query Match 98.4%; Score 854; DB 16; Length 174;
 Best Local Similarity 98.3%; Pred. No. 3.8e-63;
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALALPAAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
 DB 61 FAVDYTRYKKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
 QY 121 SQTSTGLGVLGVSAYAVTPNVDLDAGRYNYIGKNTYKKNVRSGLSVGRVKE 174
 DB 121 SQTSTGLGVLGVSAYAVTPNVDLDAGRYNYIGKNTYKKNVRSGLSVGRVKE 174

RESULT 5

Q9RP16 PRELIMINARY; PRT; 174 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE SURFACE PROTEIN A.
 GN NSPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NG3/88;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains."
 RL Infect. Immun. 0:0-0(1999).
 DR EMBL; AF175681; AAD53284.1; -.
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity: 1.
 SQ SEQUENCE 174 AA; 18355 MW; ECF6F38B9286800E CRC64;

Query Match 98.2%; Score 852; DB 2; Length 174;
 Best Local Similarity 97.7%; Pred. No. 5.6e-63;
 Matches 170; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALALPAAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
 DB 61 FAVDYTRYKKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
 QY 121 SQTSTGLGVLGVSAYAVTPNVDLDAGRYNYIGKNTYKKNVRSGLSVGRVKE 174
 DB 121 SQTSTGLGVLGVSAYAVTPNVDLDAGRYNYIGKNTYKKNVRSGLSVGRVKE 174

RESULT 6

Q9RP18 PRELIMINARY; PRT; 174 AA.

AC Q9RP18: 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE SURFACE PROTEIN A.
 GN NSPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-8047;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains."
 RL Infect. Immun. 0:0-0(1999).
 DR EMBL; AF175676; AAD53279.1; -.
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity: 1.
 SQ SEQUENCE 174 AA; 18357 MW; 0205A1DA1B7F005 CRC64;

Query Match 97.5%; Score 846; DB 2; Length 174;
 Best Local Similarity 97.1%; Pred. No. 1.7e-62;
 Matches 169; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKKALATLIALALPAAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
 DB 61 FAVDYTRYKKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
 QY 121 SQTSTGLGVLGVSAYAVTPNVDLDAGRYNYIGKNTYKKNVRSGLSVGRVKE 174
 DB 121 SQTSTGLGVLGVSAYAVTPNVDLDAGRYNYIGKNTYKKNVRSGLSVGRVKE 174

RESULT 7

P95343 PRELIMINARY; PRT; 174 AA.

DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE OUTER MEMBRANE PROTEIN PRECURSOR.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B2;
 RC MEDLINE=99270944; PubMed=10338491;
 RA Plante M., Cadieux N., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
 RT "Antigenic and molecular conservation of the gonococcal NSPA protein."
 RL Infect. Immun. 67:2855-2861(1999).
 DR EMBL; U52069; AAB41581.1; -.
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity: 1.
 KW SIGNAL.
 FT SIGNAL.
 SQ SEQUENCE 174 AA; 18337 MW; 1B558EC9A040841A CRC64;

Query Match 95.0%; Score 825; DB 2; Length 174;
 Best Local Similarity 94.3%; Pred. No. 9.5e-61;
 Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKKALATLIALALPAAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
 DB 61 FAVDYTRYKKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120

OY 121 SOTSIGLVLTGVSVAATPVNDLDAGRYRYIKGVNTVKNVSGELSGVRYKF 174
 DB 121 SKTSAGLVLAGVSVAATPVNDLDAGRYRYIKGVNTVKNVSGELSGVRYKF 174

RESULT 8

P95371 PRELIMINARY; PRT; 175 AA.
 AC P95371;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE OUTER MEMBRANE PROTEIN PRECURSOR.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MCH 88;
 RX MEDLINE=99386904; PubMed=10456958;
 RA Cadieux N., Plante M., Rioux C.R., Brodeur B.R., Martin D.;
 RT "Bactericidal and cross-protective activities of a monoclonal antibody
 directed against Neisseria meningitidis Nspa outer membrane protein.";
 RL Infect. Immun. 67:4955-4959(1999).
 DR EMBL: U52067; AAB41579.1; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KM Signal.
 FT SIGNAL 1 19 POTENTIAL.
 SQ SEQUENCE 175 AA; 18572 MW; 18582F2F5CC2FEA CRC64;

Query Match 95.0%; Score 824.5; DB 2; Length 175;
 Best Local Similarity 95.4%; Pred. No. 1.1e-60;
 Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

OY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSSLGSAKGSPPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSSLGSAKGSPPRISAGYRINDLR 60
 OY 61 FAVDYTRYKKNK-APSTDFKLSIGASAIYDFDQSPVKPYLGARLSLNFRASVDLGSSDS 119
 DB 61 FAVDYTRYKKNKQVPSDFKLSIGASAIYDFDQSPVKPYLGARLSLNFRASVDLGSSDS 120
 OY 120 FSGTSGIGLVLTGVSVAATPVNDLDAGRYRYIKGVNTVKNVSGELSGVRYKF 174
 DB 121 FSGTSGIGLVLAGVSVAATPVNDLDAGRYRYIKGVNTVKNVSGELSGVRYKF 175

RESULT 9

O51124 PRELIMINARY; PRT; 256 AA.
 AC O51124;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE OPACTY OUTERMEMBRANE PROTEIN (FRAGMENT).
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=24197;
 RX MEDLINE=98129089; PubMed=9467908;
 RA Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecek B.,
 RT "Recombinational reassortment among opa genes from ET-37 complex
 Neisseria meningitidis isolates of diverse geographical origins.";
 RL Microbiology 144:157-166(1998).
 DR EMBL: U37255; AAC46101.1; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.

FT NON_TER 1 1
 SQ SEQUENCE 256 AA; 28335 MW; 9D41C6079C6DD13F CRC64;

Query Match 28.5%; Score 247; DB 2; Length 256;
 Best Local Similarity 32.3%; Pred. No. 8.3e-13;
 Matches 69; Conservative 32; Mismatches 64; Indels 78; Gaps 7;

OY 8 LIALPAAALAEAGSGFYVQADAAHAKASSSLGSAKGSPPRISAGYRINDLR 47
 DB 14 LESSAQAASDESDSGHGPYVQADLAVERITHDYPKATGANNSTVSDFRNRIRASIH 73
 OY 48 PRISAGYRINDLRVNDYTRYK-----NYKAPSTDFK-----LYS 82
 DB 74 PVSAGYDFGGMRIADYASRYKMKESNSYKVTEDIANDKETKTEHOQNSFHAASS 133
 OY 83 IGASAIYDFDQSPVKPYLGARLSLNFRASVDLGSSDS 116
 DB 134 LGLSALYDFKLNDRKPYLGARVAAGHYKHQVSEYKTTVTSKPATSPQGGPIIQTQD 193
 OY 117 -----SDSFGTSGIGLVLTGVSVAATPVNDLDAGRYRYIKGVNTVKNVSGELSGV 170
 DB 194 PCKPYHSHSISLGLVLAGVGFDTIPKLTLDTRYRHNWGRLENTFR-FKTHEVSLGM 252
 OY 171 RYKF 174
 DB 253 RYKF 256

RESULT 10

O9CM19 PRELIMINARY; PRT; 186 AA.

OY 09CM19;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE OPA.
 GN OPA OR PM1025.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Pasteurella.
 NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PM70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida Pm70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 DR EMBL: AE06143; AAK03109.1; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KM Complete proteome.
 SQ SEQUENCE 186 AA; 20512 MW; 1B17F0A4AFC0157 CRC64;

Query Match 28.4%; Score 246.5; DB 16; Length 186;
 Best Local Similarity 32.3%; Pred. No. 6.2e-13;
 Matches 61; Conservative 32; Mismatches 77; Indels 19; Gaps 5;

OY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSSLGSAKGSPPRISAGYRIN 57
 DB 2 MKK---SLVLAIGALCSLTASANFVQDGLGAKTKSSYEMNKRTIVNVSVDLG 58
 OY 58 DLRFANDYTRYKKNKAPS-----TDFKLSIGASAIYDFDQSPVKPYLGARLSLN 108
 DB 59 AMRLADYTHYGFSGTSTFGVNOKEHSTKLYGLSLAFDENINSVLKPYVGRRLASN 118
 OY 109 RASVDLGSSDSF---SOTSIGLVLTGVSVAATPVNDLDAGRYRYIKGVNTVKNVSGE 165
 DB 119 IPIENKGSNFRSEKTKTLGIGFLIAGAYGLMTNLFVNGGLEIYRRLGRFSDT-SYNGYG 177
 OY 166 LSYGVRYKF 174
 DB 178 AKVGLRYDF 186

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RESULT 11
Q9R719 PRELIMINARY; PRT; 234 AA.
AC 09R719;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE OPACITY PROTEIN (FRAGMENT).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=23906;
RX MEDLINE=98010345; PubMed=9350862;
RA Morelli G., Malorny B., Mueller K., Sella A., Wang J., del Valle J.,
RA Achman M.,
RT "Clonal descent and microevolution of Neisseria meningitidis during 30
RT years of epidemic spread."
RL Mol. Microbiol. 25:1047-1064(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=3926;
RA Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Linz B.,
RA Popovic T., Schutman I.G.A., Adegoke R.A., Zurch K., Gagneux S.,
RA Platonov A.E., Riou J.Y., Gaugant D.A., Nicolas P., Achman M.,
RT "Genotypes and escape variants of subgroup III Neisseria
RT meningitidis during three pandemics of epidemic meningitis."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF001194; AAC32715.1; -
DR EMBL: AJ292235; CAC36358.1; -
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity; 1.
FT NON_TER 1
SQ SEQUENCE 234 AA; 26161 MW; F97142F463136EC1 CRC64;

Query Match 28.1%; Score 244; DB 2; Length 234;
Best Local Similarity 28.9%; Pred. No. 1.3e-12;
Matches 67; Conservative 32; Mismatches 59; Indels 74; Gaps 8;

QY 16 AALAEAG-SGEYVQADAAH-----AKSSSLGSG-----AKGSPRISAGY 54
DB 4 AASEDGSRSPPYVQADLAIAERITHDYPOATGANNSTVSDYFRNIRASHIPRVSVGY 63
QY 55 RINDLRFAVDYTRYK-----NYKAPSTDFK-----LYSIGASAI 88
DB 64 DFGDMRIADYASYRKKESSNYSKYTEFKHONGKQEDKTEHOGSGFHAISLGLSAI 123
QY 89 YPDFDQSPYKPYIGARLSINR-----ASVDLGG-----SDSFSQ 122
DB 124 YDFKLSDFKPYIGARVAGHVKHGVHVESKTTVTNNNGPVPPOGTPPKPAVHESHSHI 183
QY 123 TSIGLGLTVGSYAVTPNVNLDAGRYNYIKGVNTVKVRSGELSGVGRVKE 174
DB 184 SSVGLGVAGVGFDTIRKLTLDGTGRYHNMWGLENTFR-KTHHEVSLGMRHYF 234

RESULT 12
007280
ID 007280 PRELIMINARY; PRT; 234 AA.
AC 007280;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE OPACITY PROTEIN (FRAGMENT).
GN OPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=23524;
RX MEDLINE=98010345; PubMed=9350862;
RA Morelli G., Malorny B., Muller K., Sella A., Wang J.F., del Valle J.,
RA Achman M.,
RT "Clonal descent and microevolution of Neisseria meningitidis during 30
RT years of epidemic spread."
RL Mol. Microbiol. 25:1047-1064(1997).
DR EMBL: AF001195; AAC32716.1; -
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity; 1.
FT NON_TER 1
SQ SEQUENCE 234 AA; 26134 MW; 005AD356E93BC50 CRC64;

Query Match 28.1%; Score 244; DB 2; Length 234;
Best Local Similarity 28.9%; Pred. No. 1.3e-12;
Matches 67; Conservative 32; Mismatches 59; Indels 74; Gaps 8;

QY 16 AALAEAG-SGEYVQADAAH-----AKSSSLGSG-----AKGSPRISAGY 54
DB 4 AASEDGSRSPPYVQADLAIAERITHDYPOATGANNSTVSDYFRNIRASHIPRVSVGY 63
QY 55 RINDLRFAVDYTRYK-----NYKAPSTDFK-----LYSIGASAI 88
DB 64 DFGDMRIADYASYRKKESSNYSKYTEFKHONGKQEDKTEHOGSGFHAISLGLSAI 123
QY 89 YPDFDQSPYKPYIGARLSINR-----ASVDLGG-----SDSFSQ 122
DB 124 YDFKLSDFKPYIGARVAGHVKHGVHVESKTTVTNNNGPVPPOGTPPKPAVHESHSHI 183
QY 123 TSIGLGLTVGSYAVTPNVNLDAGRYNYIKGVNTVKVRSGELSGVGRVKE 174
DB 184 SSVGLGVAGVGFDTIRKLTLDGTGRYHNMWGLENTFR-KTHHEVSLGMRHYF 234

RESULT 13
Q9R718 PRELIMINARY; PRT; 234 AA.
AC 09R718;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE OPACITY PROTEIN (FRAGMENT).
GN OPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BI;
RX MEDLINE=98010345; PubMed=9350862;
RA Morelli G., Malorny B., Muller K., Sella A., Wang J.F., del Valle J.,
RA Achman M.,
RT "Clonal descent and microevolution of Neisseria meningitidis during 30
RT years of epidemic spread."
RL Mol. Microbiol. 25:1047-1064(1997).
DR EMBL: AF001196; AAC32717.1; -
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity; 1.
FT NON_TER 1
SQ SEQUENCE 234 AA; 26191 MW; F01D3B9163066171 CRC64;

Query Match 28.0%; Score 243; DB 2; Length 234;
Best Local Similarity 28.9%; Pred. No. 1.6e-12;
Matches 67; Conservative 31; Mismatches 60; Indels 74; Gaps 8;

QY 16 AALAEAG-SGEYVQADAAH-----AKSSSLGSG-----AKGSPRISAGY 54
DB 4 AASEDGSRSPPYVQADLAIAERITHDYPOATGANNSTVSDYFRNIRASHIPRVSVGY 63
QY 55 RINDLRFAVDYTRYK-----NYKAPSTDFK-----LYSIGASAI 88
DB 64 DFGDMRIADYASYRKKESSNYSKYTEFKHONGKQEDKTEHOGSGFHAISLGLSAI 123

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OY 89 YDEDTOSPVKPYIGARLSNR-----ASVDLG-----SDSFQ 122
DB 124 YDEKLNDRKPKPYIGVAVAGHVKHQVHVSSEKTTVTNNGGPVGPPPKPKPAYEHSBI 183
OY 123 TSGTGLVLTGVSAAVPPNDLDAGRYNYIKVNTYKNNRSGELSGVRYKF 174
DB 184 SSVGLGVAVGVGDTTPKLLDTGYRYHWMGRLENTR-FKTHEVSLGMRYHF 234

RESULT 14
OY 09K4T9 PRELIMINARY; PRT; 232 AA.
AC 09K4T9;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE OPA PROTEIN PRECURSOR (FRAGMENT).
GN OPA.
OS Neisseria lactamica.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=486;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS01;
RA Toleman M.A., Aho E., Virji M.;
RT "Antigenic relatedness of commensal and pathogenic neisserial adhesins
RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ288888; CAB93949.1; -
DR InterPro: IPR003394; Opacity: 1.
DR Pfam: PF02462; Opacity: 1.
KW Signal.
FT NON_TER 1 1 POTENTIAL.
FT SIGNAL <1 13 OPA A PROTEIN.
FT CHAIN 14 >232
FT NON_TER 232 232
SQ SEQUENCE 232 AA; 26094 MW; 36FAAE60A3C014AF CRC64;

Query Match 27.8%; Score 241.5; DB 2; Length 232;
Best Local Similarity 30.4%; Pred. No. 2.1e-12;
Matches 70; Conservative 31; Mismatches 64; Indels 65; Gaps 8;

OY 6 ATTIALLPAAALAEAGSGFYQADAAHAKASSL-----GSAGFS-----PRT 50
DB 3 SSILFSSAVQAAEDNGRPGYQADLTAYEHITHDYPGNNAKLFDDYRDVKTRSTHPR 62
OY 51 SAGYRINDLRFAVDYTRYKNY-----APSTD---FKLXS-IG 84
DB 63 SVGDFGNWRIALDYARYNNKKHGHKIRTEONKSVONGTSVKLLADHTDKGTFRKESNYG 122
OY 85 ASATYDFDTOSPVKPYIGARLSNR-----ASVDLG-----SDSFS 121
DB 123 ISATYDFDTGTRFKPYGARVGLGKIRHSTALEDKAEIIGNIPSGGLKDAHPPIHESHS 182
OY 122 QTSIGLVLTGVSAAVPPNDLDAGRYNYIKVNTYKNNRSGELSGVRYKF 171
DB 183 IRRVGFAGVAVGIDITPNTLDTGYRYHWMGRLENTR-FKTHEASLGMR 231

RESULT 15
OY 09AE80 PRELIMINARY; PRT; 241 AA.
AC 09AE80;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE OPA CITY PROTEIN (FRAGMENT).
GN OPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=29620;
RX MEDLINE=21221108; PubMed=11287631;
RA Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Bodo L.,
RA Popovic T., Schuurman I.G.A., Adegola R.A., Zurch K., Gagneux S.,
RA Platonov A.E., Riou J.Y., Gaugant D.A., Nicolas P., Achtman M.;
RT "Fit genotypes and escape variants of subgroup III Neisseria
RT meningitidis during three pandemics of epidemic meningitis.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:5234-5239(2001).
DR EMBL: AJ292238; CAC36361.1; -
DR InterPro: IPR003394; Opacity: 1.
DR Pfam: PF02462; Opacity: 1.
FT NON_TER 1 1
FT SEQUENCE 241 AA; 26923 MW; 4923ACF9484BF183 CRC64;

Query Match 27.8%; Score 241.5; DB 2; Length 241;
Best Local Similarity 28.9%; Pred. No. 2.2e-12;
Matches 69; Conservative 33; Mismatches 56; Indels 81; Gaps 8;

OY 16 AALAEGA-SGFYQADAAH-----KASSLSG-----AKGSPRISAGY 54
DB 4 AASEDGSRSPPYQADLAERITHDYPKASGANNTSYSDYTRNIRAHSHPRSVGY 63
OY 55 RINDLRFAVDYTRYKNY-----KAPSTDFFKLXSIGAS 86
DB 64 DEGDWRIALADYARKMNDKYSVTKNVQYKNGNRQDLKTENGEGTFHAYSLGLS 123
OY 87 AIVDFDTOSPVKPYIGARLSNR-----RASVDL-----GGS----- 117
DB 124 AIVDFDTGSRFPYAGVAVAGHVRHSIDSTKKTNTNLVPTNIPGSPRTIYNGSTODA 183
OY 118 --DSFSQTSIGLVLTGVSAAVPPNDLDAGRYNYIKVNTYKNNRSGELSGVRYKF 174
DB 184 YHESHIRRLGLGVAVGVGDTTPKLLDTGYRYHWMGRLENTR-FKTHEVSLGMRYHF 241

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Search completed: October 28, 2002, 16:02:38
Job time : 22.9713 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:55:03 ; Search time 24.8565 Seconds

(without alignments)
782.004 Million cell updates/sec

Title: US-09-684-883-4

Perfect score: 874
Sequence: 1 MKRALALALALPAAALAE.....VNTKVRSGEISAGVRYKF 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	874	100.0	175	AAW04892	Proteinase K resis
2	838.5	95.9	174	AAW04893	Proteinase K resis
3	824.5	94.3	174	AAW04891	Proteinase K resis
4	813.5	93.1	174	AAW04894	Proteinase K resis
5	746.5	85.4	155	AA19895	Neisseria meningit
6	138.5	15.8	170	AA173911	Neisseria meningit
7	118.5	13.6	25	AAW04912	N. meningitidis 60
8	99.5	11.4	257	AAU38252	Salmonella typhi c
9	95.5	10.9	212	AAU34556	E. coli cellular p
10	95.5	10.9	359	AA186294	Non-typhable Haem
11	95.5	10.9	568	AA186210	AIL protein-maltos

12	93.5	10.7	350	9	AA182053
13	93.5	10.7	350	22	AA1859179
14	93.5	10.7	353	22	AA1847447
15	93.5	10.7	369	21	AA1844589
16	93.5	10.7	369	21	AA196098
17	93.5	10.7	369	21	AA196098
18	91	10.4	162	17	AA196207
19	90	10.3	215	21	AA196096
20	90	10.3	215	21	AA196096
21	89.5	10.2	500	22	AA185766
22	87.5	10.0	639	22	AA187654
23	87	10.0	325	21	AA197281
24	86	9.8	282	19	AA1851090
25	86	9.8	282	21	AA185184
26	86	9.8	282	22	AA185184
27	86	9.8	286	17	AA185566
28	86	9.8	325	17	AA185565
29	86	9.8	332	18	AA1852418
30	86	9.8	332	18	AA1852418
31	86	9.8	332	19	AA1852418
32	86	9.8	332	19	AA1852418
33	86	9.8	332	20	AA1852418
34	86	9.8	332	20	AA1852418
35	86	9.8	332	22	AA1852418
36	86	9.8	364	21	AA1852418
37	86	9.8	364	21	AA1852418
38	86	9.8	364	21	AA1852418
39	86	9.8	652	20	AA1852418
40	86	9.8	652	20	AA1852418
41	86	9.8	802	19	AA1852418
42	86	9.8	802	19	AA1852418
43	86	9.8	802	20	AA1852418
44	86	9.8	802	20	AA1852418
45	86	9.8	802	20	AA1852418

ALIGNMENTS

RESULT 1
AAW04892
ID AAW04892 standard; Protein: 175 AA.
AC AAW04892;
DT 22-DEC-1996 (first entry)
DE Proteinase K resistant N. meningitidis 22 kd surface protein.
KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
XX
OS Neisseria meningitidis strain MCH88.
XX
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= sig_peptide
FT 20..175
FT /label= mat_protein
XX
XX W09629412-A1.
XX
XX 26-SEP-1996.
XX
XX 15-MAR-1996: 96MO-CA00157.
XX
XX 04-AUG-1995: 95US-0001983.
XX
XX 17-MAR-1995: 95US-0406362.
XX
XX (IAFB-) IAF BIO VAC INC.
XX
XX Brodeur BR, Hamel J, Martin D, Rioux C;

Outer membrane pro
Protein associated
MOMP p5. Hemophi
Virulence gene pro
Actinobacillus ple
Actinobacillus ple
Attachment-invasio
Actinobacillus ple
Cysteine protease
Novel human diagno
Fibronectin attach
Anaplasma marginal
Major antigenic pr
Mycobacterium tube
Mycobacterium tube
Mycobacterium tube
M. tuberculosis im
M. tuberculosis an
M. tuberculosis re
M. tuberculosis DP
Virulence gene pro
Actinobacillus ple
Actinobacillus ple
M. tuberculosis fu
M. tuberculosis fu
Mycobacterium tube
Mycobacterium tube
M. tuberculosis fu

DR WPI: 1996-443187/44.
 DR N-PSDB: AAT39040.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7: Fig 8; 117pp; English.
 XX
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 XX
 SQ Sequence 175 AA;

Query Match 100.0%; Score 874; DB 17; Length 175;
 Best Local Similarity 100.0%; Pred. No. 2e-85;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKKALATLIALALPAALAEAGAGFYVQADAAHAKASSISGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAALAEAGAGFYVQADAAHAKASSISGAKGSPRISAGYRINDLR 60
 OY 61 FAVDYTRYKNYKQVSTDFEKLKYSIGASAIYDPTQSPYKPYLGARLSLNRAVDENGSDS 120
 DB 61 FAVDYTRYKNYKQVSTDFEKLKYSIGASAIYDPTQSPYKPYLGARLSLNRAVDENGSDS 120
 OY 121 FSGTSTGLGVLGAGSYAVTPNVDLDAGYRNYIGKVTYKNVRSGELSGAVRYKF 175
 DB 121 FSGTSTGLGVLGAGSYAVTPNVDLDAGYRNYIGKVTYKNVRSGELSGAVRYKF 175

RESULT 2

AAM04893
 ID AAM04893 standard; Protein; 174 AA.

XX
 AC AAM04893;

DT 22-DEC-1996 (first entry)
 XX

DE Proteinase K resistant N. meningitidis 22 kD surface protein.

XX
 KW Proteinase K resistant; Neisseria meningitidis;

KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.

XX
 OS Neisseria meningitidis strain 24063.

XX
 FH Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= sig_peptide

FT /label= mat_protein

PN WO9629412-A1.

XX 26-SEP-1996.

PF 15-MAR-1996; 96WO-CA00157.

XX 04-AUG-1995; 95US-0001983.

PR 17-MAR-1995; 95US-0406362.

XX (IAFB-) IAF BIO VAC INC.

PI Brodeur BR, Hamel J, Martin D, Rioux C;

DR WPI: 1996-443187/44.
 DR N-PSDB: AAT39041.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7: Fig 9; 117pp; English.
 XX
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 XX
 SQ Sequence 174 AA;

Query Match 95.9%; Score 838.5; DB 17; Length 174;
 Best Local Similarity 97.1%; Pred. No. 1.2e-81;
 Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY 1 MKKALATLIALALPAALAEAGAGFYVQADAAHAKASSISGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAALAEAGAGFYVQADAAHAKASSISGAKGSPRISAGYRINDLR 60
 OY 61 FAVDYTRYKNYKQVSTDFEKLKYSIGASAIYDPTQSPYKPYLGARLSLNRAVDENGSDS 120
 DB 61 FAVDYTRYKNYKQVSTDFEKLKYSIGASAIYDPTQSPYKPYLGARLSLNRAVDENGSDS 119
 OY 121 FSGTSTGLGVLGAGSYAVTPNVDLDAGYRNYIGKVTYKNVRSGELSGAVRYKF 175
 DB 120 FSGTSTGLGVLGAGSYAVTPNVDLDAGYRNYIGKVTYKNVRSGELSGAVRYKF 174

RESULT 3

AAM04891
 ID AAM04891 standard; Protein; 174 AA.

XX
 AC AAM04891;

DT 22-DEC-1996 (first entry)
 XX

DE Proteinase K resistant N. meningitidis 22 kD surface protein.

XX
 KW Proteinase K resistant; Neisseria meningitidis;

KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.

XX
 OS Neisseria meningitidis strain 608B.

XX
 FH Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= sig_peptide

FT /label= mat_protein

PN WO9629412-A1.

XX 26-SEP-1996.

PF 15-MAR-1996; 96WO-CA00157.

XX 04-AUG-1995; 95US-0001983.

PR 17-MAR-1995; 95US-0406362.

XX (IAFB-) IAF BIO VAC INC.

PI Brodeur BR, Hamel J, Martin D, Rioux C;

DR WPI: 1996-443187/44.
 DR N-PSDB: AAT39039.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 1; 117pp; English.
 XX
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 XX
 SQ Sequence 174 AA;

Query Match 94.3%; Score 824.5; DB 17; Length 174;
 Best Local Similarity 95.4%; Pred. No. 3.9e-80;
 Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

OY 1 MKKALALIALALPAALAEAGSGFYVOADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALALIALALPAALAEAGSGFYVOADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 OY 61 FAVDYTRYKKNYKQVPSIDFKLYSIGASAIYDFDTPQSPKPYFGARLSLNRASVDLGGSDS 120
 DB 61 FAVDYTRYKKNYK-APSTDFKLYSIGASAIYDFDTPQSPKPYFGARLSLNRASVDLGGSDS 119
 OY 121 FSQSTGLGVLAGSVYATPVNDLADAGRYNYIGKVNFKNVRSGELSGAYRKF 175
 DB 120 FSQSTGLGVLAGSVYATPVNDLADAGRYNYIGKVNFKNVRSGELSGAYRKF 174

RESULT 4
 AAM04894

ID AAM04894 standard; Protein; 174 AA.

AC AAM04894;

DT 22-DEC-1996 (first entry)

DE Proteinase K resistant N. meningitidis 22 kD surface protein.

KM Proteinase K resistant; Neisseria meningitidis;

KM Neisseria gonorrhoeae; antibody; detection; probe; surface protein.

OS Neisseria meningitidis strain b2.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label-sig_peptide

FT /label=mat_protein

PN W09629412-A1.

PD 26-SEP-1996.

PF 15-MAR-1996; 96WO-CA00157.

PR 04-AUG-1995; 95US-0001983.

PR 17-MAR-1995; 95US-0406362.

PA (IAFB-) IAF BIO VAC INC.

PI Brodeur BR, Hamel J, Martin D, Rioux C;

DR WPI: 1996-443187/44.
 DR N-PSDB: AAT39042.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 10; 117pp; English.
 XX
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 XX
 SQ Sequence 174 AA;

Query Match 93.1%; Score 813.5; DB 17; Length 174;
 Best Local Similarity 93.7%; Pred. No. 5.9e-79;
 Matches 164; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

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 DB 1 MKKALALIALALPAALAEAGSGFYVOADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 OY 61 FAVDYTRYKKNYKQVPSIDFKLYSIGASAIYDFDTPQSPKPYFGARLSLNRASVDLGGSDS 120
 DB 61 FAVDYTRYKKNYK-APSTDFKLYSIGASAIYDFDTPQSPKPYFGARLSLNRASVDLGGSDS 119
 OY 121 FSQSTGLGVLAGSVYATPVNDLADAGRYNYIGKVNFKNVRSGELSGAYRKF 175
 DB 120 FSQSTGLGVLAGSVYATPVNDLADAGRYNYIGKVNFKNVRSGELSGAYRKF 174

RESULT 5
 AAB19895

ID AAB19895 standard; Protein; 155 AA.

AC AAB19895;

DT 19-MAR-2001 (first entry)

DE Neisseria meningitidis Neppa protein.

KM Neppa; infection; diagnosis; therapy; vaccine; meningococcal B.

OS Neisseria meningitidis.

XX Key Location/Qualifiers

FT Region 6..17 "transmembrane beta-strand"

FT Region 18..26 "surface-exposed connecting loop"

FT Region 27..37 "transmembrane beta-strand"

FT Region 40..50 "transmembrane beta-strand"

FT Region 51..62 "transmembrane beta-strand"

FT Region 63..74 "surface-exposed connecting loop"

FT Region 78..88 "transmembrane beta-strand"

FT Region 89..104 "transmembrane beta-strand"

FT Region 105..114 "surface-exposed connecting loop"

FT Region 118..130 "transmembrane beta-strand"

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FT  /note="transmembrane beta-strand"
FT  131..145
FT  /note="surface-exposed connecting loop"
FT  146..155
FT  Region
FT  /note="transmembrane beta-strand"
XX  WO20007125-A2.
XX  30-NOV-2000.
XX  19-MAY-2000; 2000WO-IB00828.
XX  19-MAY-1999; 99GB-0011692.
XX  19-AUG-1999; 99GB-0019705.
XX  09-MAR-2000; 2000GB-0005730.
XX  (CHIR-) CHIRON SPA.
XX  Glutiant MM, Pizaa M, Rappuoli R;
XX  WPI: 2001-025167/03.
XX  Novel composition comprising first and second biological molecules from
XX  a Neisseria bacterium, useful as vaccines or immunogenic compositions
XX  for treating Neisserial infections
XX  Example 12; Fig 32; 126pp; English.
XX  The present sequence is that of the Neisseria meningitidis NspA
XX  protein, which contains 8 transmembrane beta-strands and 4
XX  surface-exposed connected loops. Recombinant NspA is being
XX  developed as a vaccine for the prevention of meningococcal
XX  disease caused by all serotypes. The invention provides
XX  combination compositions comprising: (i) 2 or more Neisserial
XX  proteins, (ii) 2 or more different Neisserial nucleic acids; or
XX  (iii) mixtures of 1 or more Neisserial protein and 1 or more
XX  Neisserial nucleic acid. The proteins and nucleic acids are
XX  preferably from different Neisseria spp., especially Neisseria
XX  meningitidis and Neisseria gonorrhoeae, but may be from the same
XX  species. A claimed composition includes the NspA protein,
XX  preferably in mature form. The compositions are used e.g. as
XX  immunogenic compositions, vaccines or diagnostic reagents. They
XX  are used to treat or prevent Neisserial infection, to detect the
XX  presence of Neisserial bacteria or of antibodies raised against
XX  Neisserial bacteria, and/or as reagents which can raise antibodies
XX  against Neisserial bacteria.
XX  Sequence 155 AA;
XX  Query Match 85.4%; Score 746.5; DB 22; Length 155;
XX  Best Local Similarity 95.5%; Pred. No. 7.3e-72;
XX  Matches 149; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
XX  20 EGASGFYQADAAHAKKASSLSGSAKGFSPRISAGRIINDLFAVDYTRKYNKQVPSNDF 79
XX  1 EGASGFYQADAAHAKKASSLSGSAKGFSPRISAGRIINDLFAVDYTRKYNK APTDF 59
XX  80 KLYSIGASAIYDEPTQSPVRYKPYLGARLSLNRAVDENGSDSFSQSTGLGVLAGVSYAVT 139
XX  60 KLYSIGASAIYDEPTQSPVRYKPYLGARLSLNRAVDLGGSDSFSQSTGLGVLAGVSYAVT 119
XX  140 PNVDLDAGRYNYIGKVTYKNNRSGELSGAVRYKF 175
XX  120 PNVDLDAGRYNYIGKVTYKNNRSGELSGAVRYKF 155
XX  RESULT 6
XX  AAR73911
XX  ID AAR73911 standard; protein: 170 AA.
XX  AC AAR73911;
XX  XX
XX  DT 05-DEC-1995 (first entry)

```

```

XX  Neisseria meningitidis opacity related protein POPM3.
DE  Neisseria meningitidis; opacity related protein POPM3; vaccine;
XX  Neisseria meningitidis related homologous antigenic sequence; MRHAS; RV-1;
XX  immunosassay; diagnosis; treatment; prophylactic; bacterial;
XX  viral.
XX  Neisseria meningitidis.
XX  WO9509232-A.
XX  06-APR-1995.
XX  28-SEP-1994; 94WO-CA00516.
XX  28-SEP-1993; 93US-0127499.
XX  (SHAR/) SHARMA L R.
XX  (VALS/) VAN ALSTYNE D.
XX  Sharma LR, Van Alstyne D;
XX  WPI: 1995-147431/19.
XX  New peptide(s) and corresp. antibodies for the treatment of
XX  meningitis - the peptide(s) corresp. to homologous antigenic
XX  sites on bacterial and viral agents and on chemokine(s), used for
XX  detecting and preventing meningitis
XX  Claim 47; Fig 5/10; 98pp; English.
XX  AAR73911 is the Neisseria meningitidis opacity related protein POPM3.
XX  It contains the meningitis related antigenic sequences (MRHAS)
XX  claimed in AAR73889 and AAR73901, which are recognised by a monoclonal
XX  antibody from the hybridoma Rubella virus (RV-1). The claimed MRHAS
XX  peptides may be used in immunoassays to diagnose the presence of
XX  bacterial and/or viral meningitis agents in a sample, or in
XX  prophylactic and therapeutic meningitis treatments. The peptides may
XX  also be used as vaccines against meningitis.
XX  NB: Identified by matching corresponding MRHAS peptides.
XX  Sequence 170 AA;
XX  Query Match 15.8%; Score 138.5; DB 16; Length 170;
XX  Best Local Similarity 26.9%; Pred. No. 8.5e-07;
XX  Matches 42; Conservative 19; Mismatches 48; Indels 47; Gaps 4;
XX  6 ALIALALPAAALAEAGSGFYQADAAH-----AKASSISGS-----AKG 45
XX  15 SSILFSSAAQAASEDRSPFYQADALVAAERITHDYPQATGANNSTVSDYFRNIRAHS 74
XX  46 FSPRISAGRYINDLFAVDYTRKYNK-----KQVPSDFK 80
XX  75 IHPRVSVGYDEFGSWRIAAALYASRYKNNKNSYVNTKELENKNNKDKLTENGEGTGFHA 134
XX  81 KLYSIGASAIYDEPTQSPVRYKPYLGARLSLN--RASVD 114
XX  135 ASSISGSAIYDEFTKNGKFKPYIGARVAYGVHRSID 170
XX  RESULT 7
XX  AAM04912
XX  ID AAM04912 standard; protein: 25 AA.
XX  AC AAM04912;
XX  XX
XX  DT 22-DEC-1996 (first entry)
XX  N. meningitidis 608B peptide CS-857.
XX  DE Proteinase K resistant; Neisseria meningitidis; epitope; mapping;
XX  KM Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
XX  KM

```


XX Synthetic.
OS
XX
XX WO9629412-A1.
XX
XX 26-SEP-1996.
PD
XX
XX 15-MAR-1996; 96WO-CA00157.
PF
XX
XX 04-AUG-1995; 95US-0001983.
PR
XX 17-MAR-1995; 95US-0406362.
XX
XX (IAFB-) IAF BIO VAC INC.
PA
XX Brodeur BR, Hamel J, Martin D, Rioux C;
PI WPI; 1996-443187/44.
DR
XX
XX Neisseria meningitidis antigen, highly conserved between different
PT strains - useful for prodn. of antibodies for immunisation against,
PT or diagnosis of, N. meningitidis infection
XX
XX Claim 24; Page 84; 117pp; English.
PS
XX
XX Example 9 describes the epitope mapping of the 22 kD
CC N. meningitidis protein. Identification was accomplished
CC using 18 overlapping synthetic peptides (AAW04895 to AAW04912).
CC
XX
SQ Sequence 25 AA;
Query Match 13.6%; Score 118.5; DB 17; Length 25;
Best Local Similarity 92.3%; Pred. No. 8.7e-06;
Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 61 FAVDYTRYKNYKQVSTDFKLYSICA 86
ID 1 FAVDYTRYKNYK-APSTDFKLYSICA 25
DB
RESULT 8
AAU38252
ID AAU38252 standard; Protein; 257 AA.
XX
XX AC AAU38252;
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX Salmonella typhi cellular proliferation protein #143.
DE
XX
XX Antisense; prokaryotic cellular proliferation protein;
KW antibiotic; antibacterial; drug design.
XX
XX Salmomella typhi.
OS
XX
XX WO200170955-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US09180.
PF
XX
XX 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
XX (ELITR-) ELITRA PHARM INC.
PA
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX

DR WPI; 2001-611495/70.
DR N-PSDB; AAS56111.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
PT
XX
XX Example 3; Seq ID No 13845; 511pp; English.
PS
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmomella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 257 AA;
Query Match 11.4%; Score 99.5; DB 22; Length 257;
Best Local Similarity 25.2%; Pred. No. 0.022;
Matches 55; Conservative 29; Mismatches 81; Indels 53; Gaps 12;
QY 1 MKKLAALIALA--LPAALAEAGSGFYQADAAHK-----ASSSIGSAKGFSPRSAGY 54
DB 27 MKKTTVALALITLSSGAPAHGEPFRAGPYVPTGAGCTGHLNGFD--VSNN 84
QY 55 RINDLRPAVDYTRYKNYKQVSTDFKLYSICASAIYDF-----DPQSP 97
DB 85 QLG-LFTYMATDNIGVELLAATPER-HKVGATGATGDIATVHLPTLMAQWFGSSSK 142
QY 98 VKPYLGARLSINRASV---DPNG-----SDSFSQSTGLGVLAVGYSAVTPN----- 141
DB 143 VRPYVG--VGNYVTTFEPDNDFNGKKTGLSLDFKSKGAGAGVGYDLINRDMGLGAS 200
QY 142 ---VDLDAGRYNYIGKVTNVKNVRSGE---LSAGVR 172
DB 201 VNYMDIDTTANYK-MGGVQOHDSVRLDPWVFMFSAGXR 237
RESULT 9
AAU34556
ID AAU34556 standard; Protein; 212 AA.
XX
XX AC AAU34556;
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX E. coli cellular proliferation protein #137.
DE
XX
XX Antisense; prokaryotic cellular proliferation protein;
KW antibiotic; antibacterial; drug design.
XX
XX Escherichia coli.
OS
XX
XX WO200170955-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US09180.
PF
XX 21-MAR-2000; 2000US-191078P.
PR

PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207272P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX (ELITRA) ELITRA PHARM INC.
 PA Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ,
 PI Yamamoto RT, Xu HH;
 XX WPI: 2001-611495/70.
 DR N-PSDB; AAS52415.
 XX
 XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 PS
 PS Example 3; Seq ID No 10149; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 212 AA;
 SQ
 Query Match 10.9%; Score 95.5; DB 22; Length 212;
 Best Local Similarity 24.8%; Pred. No. 0.045;
 Matches 54; Conservative 29; Mismatches 82; Indels 53; Gaps 11;
 QY 1 MKKALALIALA--LPAALAEAGSGFYQADAAHAK-----ASSSLGSAKGFSPRISAGY 54
 DB 1 MKKLTVALLAVTTLLSGSAFAHEAGFEFFMRGSAFTVRPTBGAGSTLGLGFS--VTNNT 58
 QY 55 RINDLREAVDYTRYKNKYQVPSIDFKLYSIGASAIYDF-----DTQSP 97
 DB 59 QLG-LTFEYMAVDNIGVEILLATPFR-HKIGTRATGDIATVHMLPTLMQWTFEGDASSK 116
 QY 98 VKPTIGARLSTNRASVDPNF-----SDSFQSTSTGIGVLAGSYAVTPN----- 141
 DB 117 FRPYVGA--GINTYTFEDNGFNDRGKAGSLDSLKDSWGAAQGVGDYLDINRWMLVMS 174
 QY 142 ---VDLDAGYRYNTIGKNTVKNRSGE---LSAGVR 172
 DB 175 VWYMDIDTTANYK-LGGAQCHDSVRLDPWPMFSAGTR 211
 RESULT 10
 AAR6294
 ID AAR6294 standard; Protein; 359 AA.
 AC AAR6294;
 XX
 XX 09-AUG-1995 (first entry)
 XX
 XX Non-typable Haemophilus influenza (NTHI) fimbria protein.
 DE
 XX

KW Fimbria protein; vaccine; otitis media.
 XX
 OS Haemophilus influenza strain 1128.
 XX
 FH Key Location/Qualifiers
 FT Region 22..33
 FT /Label= amino terminus
 FT Peptide 234..249
 FT /Label= internal CNBR fragment
 XX
 PN WO9426304-A.
 XX
 PD 24-NOV-1994.
 XX
 PF 12-MAY-1994; 94WO-US05477.
 XX
 PR 18-MAY-1993; 93US-0065442.
 XX
 PA (OHIO-) OHIO STATE RES FOUND.
 XX
 PI Bakaletz LO, Kolatukudy PE, Sirakova T;
 XX WPI: 1995-006359/01.
 DR N-PSDB; AAQ78916.
 XX
 PT Vaccine comprising non-typable Haemophilus influenza fimbria
 PT protein - useful in studying, preventing or reducing the
 PT severity of otitis media, also fimbria protein and DNA.
 PS Disclosure; Fig 5; 45pp; English.
 XX
 CC The fimbria proteins from 15 randomly selected type b and non-
 CC typable clinical isolates of Haemophilus influenza share common
 CC epitopes. Thus fimbria isolated from non-typable Haemophilus
 CC influenzae 1128 strain is a particularly suitable immunogen to
 CC protect against the different non-typable H₂ influenzae that cause
 CC otitis media. Fimbria protein is produced by culturing a transformed
 CC microbial host, pref. *E. coli*, *Sporodoptera frugiperda* or a mucosal
 CC pathogen. Fimbria protein (FP) produced by this process is claimed.
 CC The FP protein migrates in polyacrylamide gels to a posn. equiv. to
 CC a mol. wt. of 25.5 kD or 37.5 kD.
 XX
 XX Sequence 359 AA;
 SQ
 Query Match 10.9%; Score 95.5; DB 16; Length 359;
 Best Local Similarity 22.7%; Pred. No. 0.092;
 Matches 51; Conservative 30; Mismatches 89; Indels 55; Gaps 9;
 QY 1 MKKALALIALA--LPAALAEAG--SGFYQADAA-----HAKASSLSGSAKGFSPRISAG 53
 DB 1 MKKTAIALVAGLAAASVAQAPOENTFYAGVAGAGSGFHDGINNGAIIKKGSSS-NYG 59
 QY 54 YRINDLREAVDYTRYKNKYQVPSIDFKL-----YSIGASAIYDDDTQSPKPYIGANLS 107
 DB 60 YRNTFTTYGV-----FEGQIILNODNFGLAELGYHDFGAKLREAGKRAKHTNHGAILLS 115
 QY 108 LNRASVDPNFSDSFQSTSTGL-----GYLA-GVSYAVT 139
 DB 116 LKGSYVLDLGLDVTYAGAGVALRSDYKFEYDANGTRDHRKKGHTARASGLFVAGAEYAVL 175
 QY 140 PNVDLDAGY-----RYNTYKNTVKNRVS--GELSGAVRVP 175
 DB 176 PELAVRLLEYQWLTFRVQKYPQDKPMTAINYNPIMGICINAGISYRF 220
 RESULT 11
 AAR6210
 ID AAR6210 standard; Protein; 568 AA.
 AC AAR6210;
 XX
 XX 24-AUG-1996 (first entry)
 XX
 XX

OY 1 MKKALALIALPAAALAEGA---SGFYQADAAHAKASSSIGS-----AKGFS 47
 DB 1 MKKALALVYAGLAASVAGAPQEMTFEYAGVAKGQASPHDGLRALAREKYGHHNSFT 60
 OY 48 PRISAGYRI---NDLREAV-----DYTRYKNYKQVPSTDFKLYSIGASA--SAIDPEPTQSP 97
 DB 61 YGVEGGYQIINONNLGIAVEBELGYDDGFRAGK--REKGTIVYKHINHSTHLSLKGSTYVLEG 119
 OY 98 VKPYLGARLSLNRASVDENGSDSEFSQSTSTGLG-----VLGVSYAVTPNVDLDAG 147
 DB 120 LDVYGRAGVALVRS--DYKLYNENSSTLKKLGHHRRARASGLFVAGAEYAVLPBELAVRLE 177
 OY 148 Y-----RNYTIGKYNVTKNRS--GELSAQYRYKF 175
 DB 178 YQMLTRVGKTRPQDKPNTALNTPWIGSINAGISYRF 214

RESULT 15

AAB44589

ID AAB44589 standard: Protein; 369 AA.

AC AAB44589;

DT 08-FEB-2001 (first entry)

DE Virulence gene protein #69.

KW Virulence gene: antibacterial; vaccine; bacterial infection;

KM septicaemia; bronchopneumonia; rhinitis; wound infection.

OS Actinobacillus pleuropneumoniae.

PN W0200061724-A2.

PD 19-OCT-2000.

PF 06-APR-2000; 2000WO-US09218.

PR 09-APR-1999; 99US-0128689.

PR 10-SEP-1999; 99US-0153453.

PA (PHNA) PHARMACIA & UPJOHN INC.

PI Lowery DE, Fuller TE, Kennedy MJ;

DR WPI: 2000-647422/62.

DR N-PSDB; AAC79664.

PT Attenuated Pasteurellaceae bacteria comprising mutations in virulence
 genes, useful as a live attenuated vaccine against bacterial infections

PS Claim 39; Pages 308-309; 322pp; English.

CC The family Pasteurellaceae encompasses several pathogens that infect a
 CC wide variety of animals. The present invention relates to virulence genes
 CC from Pasteurellaceae. The present sequence is a protein encoded by one
 CC such virulence gene. The virulence genes of the present invention may be
 CC mutated in order to produce an inactive gene. The inactive virulence gene
 CC may in turn be used to produce a vaccine, which is useful for treating
 CC bacterial infections such as septicaemias, bronchopneumonias, rhinitis and
 CC wound infections.

XX Sequence 369 AA;

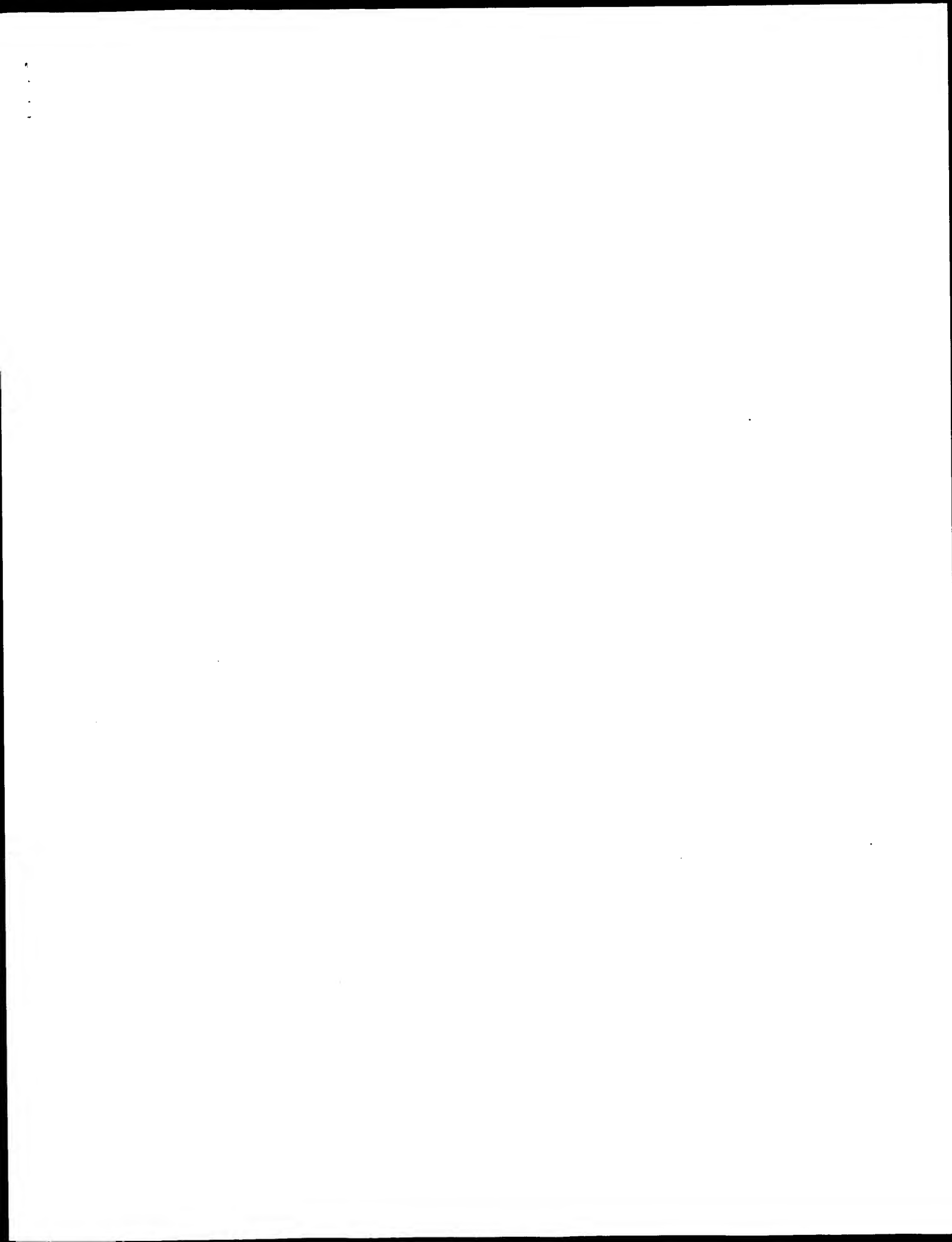
Query Match 10.7%; Score 93.5; DB 21; Length 369;

Best Local Similarity 23.2%; Pred. No. 0.16; Mismatches 78; Indels 67; Caps 12;

OY 1 MKKALALIALPAAALAEGA---SGFYQADAAHAKASSSIGSAK-GFSPRI---SAG 53
 DB 1 MKKSLVALAVYS--AAAVAGAAPOONTFYAGAKYQSSFHGYNQLKSGHDDRYNDKTRK 58

OY 54 YRINDLREAVDYTRYKNYKQVPSTDFKLYSIGASAIYDF-----DT 94
 DB 59 YGIN--RNSVTYGVYGGYQIINONNF---GLAELGTDYGRVGNNDDEFTYVHSAHGL 113
 OY 95 OSPVKEP-----YLGARLSLNRASVDENGSDSEFSQSTSTGLGVL-----AGVSYA 137
 DB 114 NLALRPSYEVLPDLIDYGRVGIAYVRNDYKKYGAEENTNESTTKFHKLKASTILGAGYEYA 173
 OY 138 VTPNVDLDAGYRYNYIGKYNVTKN--VRSG-----ELSAQYRYKF 175
 DB 174 ILP--ELARVEYQYTLNKAQNLKALVRSQYQVDVQYAPDIHSVTAGLSYRF 224

Search completed: October 28, 2002, 16:00:38
 Job time : 26.8565 secs



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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:58:54 ; Search time 9.54089 Seconds
(without alignments)
448.017 Million cell updates/sec

Title: US-09-684-883-4

Perfect score: 874
Sequence: 1 MKKALALALALPAAALAE.....VNTVKNVSGELSGAVRVK 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/Backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	874	100.0	175	4	US-08-913-362-4
2	843	96.5	175	4	US-08-913-362-30
3	838.5	95.9	174	4	US-08-913-362-6
4	824.5	94.3	174	4	US-08-913-362-2
5	813.5	93.1	174	4	US-08-913-362-8
6	138.5	15.8	170	1	US-08-127-459A-20
7	138.5	15.8	170	1	US-08-482-847-20
8	118.5	13.6	25	4	US-08-913-362-26
9	95.5	10.9	568	5	PCR-US95-13749-5
10	93.5	10.7	359	1	US-08-457-997B-2
11	93.5	10.7	359	3	US-08-467-722A-2
12	86	9.8	282	3	US-08-733-230-6
13	86	9.8	282	4	US-08-953-326-6
14	86	9.8	286	1	US-08-382-184-3
15	86	9.8	286	2	US-08-641-356-3
16	86	9.8	286	4	US-09-132-528-4
17	86	9.8	286	4	US-08-875-494-3
18	86	9.8	325	1	US-09-599-366-4
19	86	9.8	325	1	US-08-582-184-2
20	86	9.8	325	2	US-08-641-356-2
21	86	9.8	325	4	US-09-132-528-2
22	86	9.8	325	4	US-09-132-528-3
23	86	9.8	325	4	US-08-875-494-2
24	86	9.8	325	4	US-09-599-366-2
25	86	9.8	332	4	US-09-599-366-3
26	86	9.8	332	4	US-08-818-112-53
27	86	9.8	332	4	US-08-818-111-53

28	86	9.8	332	4	US-09-056-556-53	Sequence 53, Appl
29	86	9.8	802	4	US-09-056-556-214	Sequence 214, App
30	81.5	9.3	2123	4	US-08-968-685A-10	Sequence 10, Appl
31	81	9.3	15	4	US-08-913-362-23	Sequence 23, Appl
32	79.5	9.1	433	2	US-08-883-515-2	Sequence 2, Appl
33	79	9.0	15	4	US-08-913-362-18	Sequence 18, Appl
34	78.5	9.0	884	1	US-08-066-167-2	Sequence 2, Appl
35	78.5	9.0	908	1	US-08-487-890A-94	Sequence 94, Appl
36	78.5	9.0	908	2	US-08-478-483-94	Sequence 94, Appl
37	78.5	9.0	908	2	US-08-337-483-94	Sequence 94, Appl
38	78.5	9.0	908	2	US-08-478-373-94	Sequence 94, Appl
39	78.5	9.0	908	3	US-08-474-671-94	Sequence 94, Appl
40	78.5	9.0	908	3	US-08-483-577A-94	Sequence 94, Appl
41	78.5	9.0	908	3	US-08-448-194-4	Sequence 16, Appl
42	78.5	9.0	908	3	US-08-613-009A-16	Sequence 94, Appl
43	78.5	9.0	908	4	US-08-897-438-94	Sequence 94, Appl
44	78.5	9.0	908	4	US-08-867-921-4	Sequence 94, Appl
45	78.5	9.0	908	4	US-08-637-654-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1
US-08-913-362-4
Sequence 4, Application US/08913362
Patent No. 6287574
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-913-362-4
Query Match 100.0%; Score 874; DB 4; Length 175;

Best Local Similarity 100.0%; Pred. No. 4e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAGSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNKQVSPDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRSASVDLFGSDS 120
DB 61 FAVDYTRYKNKQVSPDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRSASVDLFGSDS 120

QY 121 FSQSTGLGVLAGSYAVTPNVLDAGRYNYIGKVTYVKNVRSGLSAGYRVKF 175
DB 121 FSQSTGLGVLAGSYAVTPNVLDAGRYNYIGKVTYVKNVRSGLSAGYRVKF 175

RESULT 2

US-08-913-362-30
Sequence 30, Application US/08913362
Patent No. 6287574
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-913-362-30

Query Match 96.5%; Score 843; DB 4; Length 175;

Best Local Similarity 96.6%; Pred. No. 1.4e-88;
Matches 169; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAGSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAGSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNKQVSPDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRSASVDLFGSDS 120

DB 61 FAVDYTRYKNKQVSPDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRSASVDLFGSDS 120

QY 121 FSQSTGLGVLAGSYAVTPNVLDAGRYNYIGKVTYVKNVRSGLSAGYRVKF 175
DB 121 FSQSTGLGVLAGSYAVTPNVLDAGRYNYIGKVTYVKNVRSGLSAGYRVKF 175

RESULT 3

US-08-913-362-6
Sequence 6, Application US/08913362
Patent No. 6287574
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-913-362-6

Query Match 95.9%; Score 838.5; DB 4; Length 174;
Best Local Similarity 97.1%; Pred. No. 4.5e-88;
Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAGSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAGSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNKQVSPDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRSASVDLFGSDS 120

DB 61 FAVDYTRYKNKQVSPDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRSASVDLFGSDS 119

QY 121 FSQSTGLGVLAGSYAVTPNVLDAGRYNYIGKVTYVKNVRSGLSAGYRVKF 175
DB 121 FSQSTGLGVLAGSYAVTPNVLDAGRYNYIGKVTYVKNVRSGLSAGYRVKF 175

DB 120 FSQSTGLGVLAGVSYAVTPNVLDAGRYNYIKGVNTVKNVRSGLSAGVRYKF 174

RESULT 4
US-08-913-362-2
; Sequence 2, Application US/08913362
; Patent No. 6287574

GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-362-2

Query Match 94.3%; Score 824.5; DB 4; Length 174;
Best Local Similarity 95.4%; Pred. No. 1.8e-86;
Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

DB 1 MKKALALIALALPAALALGASGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAALALGASGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

DB 61 FAVDYTRYKNYKQVSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSINRASVDLGGSDS 120
DB 61 FAVDYTRYKNYKQVSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSINRASVDLGGSDS 119

DB 121 FSQSTGLGVLAGVSYAVTPNVLDAGRYNYIKGVNTVKNVRSGLSAGVRYKF 175
DB 120 FSQSTGLGVLAGVSYAVTPNVLDAGRYNYIKGVNTVKNVRSGLSAGVRYKF 174

RESULT 5
US-08-913-362-8
; Sequence 8, Application US/08913362
; Patent No. 6287574

GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136

INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-362-8

Query Match 93.1%; Score 813.5; DB 4; Length 174;
Best Local Similarity 93.7%; Pred. No. 3.2e-85;
Matches 164; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

DB 1 MKKALALIALALPAALALGASGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAALALGASGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

DB 61 FAVDYTRYKNYKQVSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSINRASVDLGGSDS 120
DB 61 FAVDYTRYKNYKQVSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSINRASVDLGGSDS 119

DB 121 FSQSTGLGVLAGVSYAVTPNVLDAGRYNYIKGVNTVKNVRSGLSAGVRYKF 175
DB 120 FSQSTGLGVLAGVSYAVTPNVLDAGRYNYIKGVNTVKNVRSGLSAGVRYKF 174

RESULT 6
US-08-127-499A-20
; Sequence 20, Application US/08127499A
; Patent No. 5510264

GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:

REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
STRAIN: 608B
US-08-913-362-26

Query Match 13.6%; Score 118.5; DB 4; Length 25;
Best Local Similarity 92.3%; Pred. No. 4.2e-07;
Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 61 FAVDYTRYKRYKQVPSDFKLYSIGA 86
DB 1 FAVDYTRYKRYK-APSTDFKLYSIGA 25

RESULT 9
PCT-US95-13749-5
Sequence 5, Application PC/TUS9513749
GENERAL INFORMATION:
APPLICANT: Amgen Inc.
TITLE OF INVENTION: COMPOSITIONS FOR INCREASED
TITLE OF INVENTION: BIOAVAILABILITY OF ORALLY DELIVERED THERAPEUTIC AGENTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13749
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-13749-5

Query Match 10.9%; Score 95.5; DB 5; Length 568;
Best Local Similarity 26.6%; Pred. No. 0.019;
Matches 49; Conservative 29; Mismatches 71; Indels 35; Gaps 9;

QY 12 ALPAALAGASGFYQADAAHAKASSLSGSA-----KGFSPRISAGYRI 56
DB 396 SVYGRSIGRASVNY---AASESSISIGYASQSHKENGTYLLDNDPKGFN--LYRTREL 450
QY 57 NDL-----KFAVDYTRYKRYK---KQVPSDFKLYSIGASAIYDFDTQSPVKEPYLGARLSL 108
DB 451 DDNMGVYGSFAFYHQGYDFYGSNKFSGHGDVDYGVTMGSPFRINDEYSLVGLGAAGK 510
QY 109 NRASVDFNGSDSFQSTGCLGLVAGSVAVTPNVDDLACGYRNYTGKRYTVANVNSGELS 168
DB 511 VASAV-FDESISASKTSMAVY--AGVQNPDPLEPNVIDASYEYS---KIDSIK-VGTWMLG 563

QY 169 AGVR 172
DB 564 AGTR 567

RESULT 10
US-08-457-997B-2
Sequence 2, Application US/08457997B
Patent No. 576608
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,997B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Goldrick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-457-997B-2

Query Match 10.7%; Score 93.5; DB 1; Length 359;
Best Local Similarity 23.5%; Pred. No. 0.017;
Matches 54; Conservative 29; Mismatches 82; Indels 65; Gaps 11;

QY 1 MKKALALIALALPAALAEGA---SGFYQADAA---HAKASSLSGSAKGFSPRISAG 53
DB 1 MKTAIALVAVAGLAASVAAQAPQENTFYAGVKAGQGSFHDGINNCAIKGLSSS-NYG 59
QY 54 YRINDLRAVDYTRYKRYKQVPSDFKLYSIGASAIYDFD-----TQSPVKEPYL----- 102
DB 60 YRNTFTTYGV---FGGIQILNDNF-----GLAAELGYDDEFRAKLREAGKPRAKHTNH 110
QY 103 GARLSLNRASVDFNGSDSFQSTGCL-----GVLA-GV 134
DB 111 GAVLSKSYEVLGDLVYKAGVALYRSDYKFEEDANGTRDHKGGHTTARASGLRAVGA 170
QY 135 SYAVTPNVDDLACGYRNYTGKRYTVANVNSGELS 175
DB 171 EYAVLPELAVLEXYQWMLRVGKYRPODKPMTALINYPMICINAGISYRF 220

RESULT 11
US-08-467-722A-2
Sequence 2, Application US/08467722A
Patent No. 6030626
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine

```

; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calfee, Halter and Griswold
; STREET: Suite 1800 800 Superior Avenue
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 44114-2688
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,722A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Golick, Mary E.
; REGISTRATION NUMBER: 34,829
; REFERENCE/DOCKET NUMBER: 22727/00102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 622-8458
; TELEFAX: (216) 241-0816
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-722A-2

Query Match
Best Local Similarity 23.5%; Score 93.5; DB 3; Length 359;
Matches 54; Conservative 29; Mismatches 82; Indels 65; Gaps 11;

QY 1 MKKALALIALPALAALAEGA---SGFYQADAA---HAKSSSLGSAKGFSPRISG 53
DB 1 MKTALILVYAGLAASVAQAPQENTFYAGYKAGCGSPFDGINNCAIKKGLSSS-NYG 59
QY 54 YRINDLRFANDYRKYKQVPTDCKLISGASAIYDPD-----TQSPVKPYL----- 102
DB 60 YRRNTFTYGV---FGGYQLNODNF-----GLAELGIDDFGRALKRAGKPKAHTNH 110
QY 103 CARLSLRASVDENGSDSFQSTSTGL-----GVLA-GV 134
DB 111 GAVLSLKGSEVLDGLDYKAGALVRSDFKPYEDANGTRDHKGRHTARASGLPFAVGA 170
QY 135 SYAVTPVNDIDAGT-----RNYIGKVNTYKVNRS--GELSAGYRVKF 175
DB 171 EYAVLPALAVLEQWLTQVGRYPQDKPMTAINYNPMWIGCINAGISYRF 220

RESULT 12
; US-08-733-230-6
; Sequence 6, Application US/08733230
; Patent No. 6025338
; GENERAL INFORMATION:
; APPLICANT: Barbet, Anthony F.
; APPLICANT: Ganta, Roman Reddy
; APPLICANT: McGuire, Travis C.
; APPLICANT: Burridge, Michael J.
; APPLICANT: Nyika, Aceme
; APPLICANT: Rutangitwa, Fred R.
; APPLICANT: Mahan, Suman M.
; TITLE OF INVENTION: Nucleic Acid Vaccines Against
; TITLE OF INVENTION: Rickettsial Diseases and Methods of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanichik & Saliwanichik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL

```

```

; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,230
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF-167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-372-5800
; TELEFAX: 352-375-8100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 282 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-733-230-6

Query Match
Best Local Similarity 26.6%; Score 86; DB 3; Length 282;
Matches 49; Conservative 17; Mismatches 58; Indels 60; Gaps 11;

QY 20 EGAGSEFYQADAAHAKSSSLGSAKGFSPRISAGYRINDLRFV---DYTR----- 67
DB 111 DGAVGY-----SLGGAR---VELEASYR---RFATLADGQYAKSGAESLAA 150
QY 68 -----YRNYKQVPTDCKLISGASAIYD-FDTQSPVKPYLGARLSINRASVDENG 118
DB 151 ITRDANITETFYFYKIDEINTSYMLNGCYDVHTDLPVSPYCA--GIGASPVDIS-- 206
QY 119 DSFQSTSTGLGV--LAGSVAVTPVNDIDAG-----YRNYIGKVNTYKVNRSSELS 168
DB 207 ---KQVTKLAVRKGKVGISYQFTPEISLVAGFGYHGLFDESIXDIPAHNSVK--FSGEAK 261
QY 169 AGVR 172
DB 262 ASVK 265

RESULT 13
; US-08-953-326-6
; Sequence 6, Application US/08953326
; Patent No. 6251872
; GENERAL INFORMATION:
; APPLICANT: Barbet, Anthony F.
; APPLICANT: Ganta, Roman R.
; APPLICANT: McGuire, Travis C.
; APPLICANT: Burridge, Michael J.
; APPLICANT: Nyika, Aceme
; APPLICANT: Rutangitwa, Fred R.
; APPLICANT: Mahan, Suman M.
; TITLE OF INVENTION: Nucleic Acid Vaccines Against
; TITLE OF INVENTION: Animals and Humans
; FILE REFERENCE: UF-167C1
; CURRENT APPLICATION NUMBER: US/08/953,326
; CURRENT FILING DATE: 1997-10-17
; EARLIER APPLICATION NUMBER: 08/953,326
; EARLIER FILING DATE: 1997-10-17
; EARLIER APPLICATION NUMBER: 08/733,230
; EARLIER FILING DATE: 1996-10-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 282
; TYPE: PRT

```

ORGANISM: Anaplasma marginale
us-08-953-326-6

Query Match 9.8%; Score 86; DB 4; Length 282;
Best Local Similarity 26.8%; Pred. No. 0.083;
Matches 49; Conservative 17; Mismatches 58; Indels 60; Gaps 11;

QY 20 BGASGFYQADAAHAKASSISGSAKSPRISAGYRINDLRFAV-----DYTR----- 67
DB 111 DGAVG-----SLGGAR-----VELEASR-----RFATLADQGVAKSGAESLAA 150
QY 68 -----YKNVKNQVSTDFKLSIGASAIYD-FDTQSPVRYIGARLSLRASVDNGS 118
DB 151 ITRDANTETRYFVVKIDETINTVSMANGCYDVLHTDLVSPYCA--GIGASFVDIS-- 206
QY 119 DFSQSTGLGV--LAGVSYAVTPNVLDAG-----YKNYIGKVTYKNGRSGELS 168
DB 207 ---KQVTKLAYRGKVGISYQFTPEISLVAGGFYHGLFDESQKIDIPAHNSVK--FSGEAK 261
QY 169 AGVR 172
DB 262 ASVK 265

RESULT 14
US-08-382-184-3
; Sequence 3, Application US/08382184
; Patent No. 5714593
; GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: MICROBACTERIAL PROTEINS,
TITLE OF INVENTION: MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
TITLE OF INVENTION: AND FOR THE DETECTION OF TUBERCULOSIS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER &
ADDRESS: NEUSTADT, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/382,184
FILING DATE: 01-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 22640720
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOHETICAL: NO
US-08-382-184-3

Query Match 9.8%; Score 86; DB 1; Length 286;
Best Local Similarity 27.9%; Pred. No. 0.085;
Matches 43; Conservative 15; Mismatches 60; Indels 36; Gaps 7;

QY 10 ALALPAAALAEASGFYVQADAAHAKASSISGSA-----KGFSPRISAGYRINDLRFA 62

DB 82 SFALPAG-----WESDAAHFYGSALSKTTGDPFPFGQPPVA-----NDFTRIY 127

QY 63 VDYTRKKNQVSTDFKLSIGASAIYDFQSPVRYIGARLSLRASVDNGSD--- 119
DB 128 IGRLDQKLYASAETDSK-----AAARLGSDMCEFPYPPGTRINQETVSLDANGVSGSA 182

QY 120 -----SFSQSTGLG-VLAGVSYAVTPNVLDAG 147
DB 183 SYEVKFSDBSKPNGQITWGVIGSPANAP-DAG 215

RESULT 15
US-08-641-356-3
; Sequence 3, Application US/08641356
; Patent No. 5866130
; GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: MICROBACTERIAL PROTEINS,
TITLE OF INVENTION: MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
TITLE OF INVENTION: AND FOR THE DETECTION OF TUBERCULOSIS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER &
ADDRESS: NEUSTADT, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/641,356
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/382,184
FILING DATE: 01-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 22640720
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOHETICAL: NO
US-08-641-356-3

Query Match 9.8%; Score 86; DB 2; Length 286;
Best Local Similarity 27.9%; Pred. No. 0.085;
Matches 43; Conservative 15; Mismatches 60; Indels 36; Gaps 7;

QY 10 ALALPAAALAEASGFYVQADAAHAKASSISGSA-----KGFSPRISAGYRINDLRFA 62
DB 82 SFALPAG-----WESDAAHFYGSALSKTTGDPFPFGQPPVA-----NDFTRIY 127

QY 63 VDYTRKKNQVSTDFKLSIGASAIYDFQSPVRYIGARLSLRASVDNGSD--- 119
DB 128 IGRLDQKLYASAETDSK-----AAARLGSDMCEFPYPPGTRINQETVSLDANGVSGSA 182

QY 120 -----SFSQSTGLG-VLAGVSYAVTPNVLDAG 147

Tue Oct 29 09:23:11 2002

us-09-684-883-4.ra1

Page 8

Db 183 SYEYKFSDDPKPNCQIWTGVIISPANAP-DAG 215

Search completed: October 28, 2002, 16:04:19
Job time : 10.5409 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:58:04 ; Search time 12.5538 Seconds

(without alignments)
1339.485 Million cell updates/sec

Title: US-09-684-883-4

Sequence: 1 MKKALALIALALPAALAE.....VTVKKNVSGELSGAVRYKF 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	838.5	95.9	174	2	B81932
2	828.5	94.8	174	2	G81174
3	245.5	27.9	260	2	SI6611
4	242	27.7	261	2	SI6610
5	241.5	27.6	283	2	S72343
6	240.5	27.5	258	2	SI6612
7	240	27.5	237	2	S36343
8	240	27.5	338	2	SI6613
9	239.5	27.4	254	2	S20043
10	239	27.3	257	2	SI6614
11	239	27.3	268	1	KONH2C
12	238.5	27.3	233	2	S36350
13	237.5	27.2	260	1	KONH0
14	237.5	27.2	266	2	SI6616
15	236.5	27.1	178	2	F64124
16	235.5	26.9	270	2	S04380
17	234.5	26.8	261	2	SI6619
18	231	26.4	234	2	S36329
19	231	26.4	282	2	SI6617
20	230.5	26.4	234	2	S36342
21	230.5	26.4	234	2	S36341
22	229.5	26.3	238	2	S36349
23	226.5	25.9	258	2	S08514
24	224.5	25.7	234	1	KONH8
25	224.5	25.7	234	2	S36348
26	223	25.5	243	2	S36346
27	222.5	25.5	243	2	S36344
28	219.5	25.1	248	2	P10038
29	210.5	24.1	239	2	S28630

30	208	23.8	247	2	S28632	opacity protein op
31	206	23.6	214	2	S44706	opacity protein op
32	196	22.4	235	2	S44707	opacity protein op
33	181	20.7	121	2	I64187	opacity protein ho
34	153	17.5	210	2	S77737	opacity protein op
35	142.5	16.3	187	2	S20044	opacity protein op
36	138.5	15.8	168	2	S08513	opacity protein-re
37	138.5	15.8	170	2	T10256	opacity protein-re
38	129.5	14.8	192	2	S44712	opacity protein-re
39	128.5	14.7	239	2	AH0541	opacity protein-re
40	128	14.6	281	2	AH3012	outer surface prot
41	128	14.6	284	2	G98271	hypothetical prote
42	126	14.4	201	2	S16286	opacity protein op
43	124.5	14.2	284	2	AC3556	heat resistant agg
44	122.5	14.0	70	2	F64066	probable outer mem
45	120	13.7	264	2	T54668	heat resistant agg

ALIGNMENTS

RESULT 1

B81932

outer membrane protein MMA0862 [imported] - Neisseria meningitidis (strain Z2491 sero

C/Species: Neisseria meningitidis

C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

C/Accession: B81932

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo

Nature 404, 502-506, 2000

A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491

A/Reference number: AB1775; MUID:20222556

A/Accession: B81932

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-174 <PAR>

A/Cross-references: GB:AL62754; GB:AL157959; NID:q7379424; PIDN:CA884143.1; PID:q737

A/Experimental source: serogroup A, strain Z2491

C/Genetics:

A/Gene: nspsA; MMA0862

Query Match 95.9%; Score 838.5; DB 2; Length 174;

Best Local Similarity 97.1%; Pred. No. 3.2e-66;

Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 MKKALALIALALPAALAEASGFYQADAAHAKSSLSGAKGSPRISAGYRINDR 60

Db 1 MKKALALIALALPAALAEASGFYQADAAHAKSSLSGAKGSPRISAGYRINDR 60

QY 61 FAVDYTRKKNYKQVSTDFKLSIGASATYDFTQSPVKPYIGARLSLRASVDENGSDS 120

Db 61 FAVDYTRKKNYK-APSDFKLSIGASATYDFTQSPVKPYIGARLSLRASVDENGSDS 119

QY 121 FSQSTGIGLVAGVSAVVPNDLDAGRYRNYGKRYNKKVNSGELSGAVRYKF 175

Db 121 FSQSTGIGLVAGVSAVVPNDLDAGRYRNYGKRYNKKVNSGELSGAVRYKF 174

RESULT 2

G81174

outer membrane protein NsgA NMB0663 [imported] - Neisseria meningitidis (strain MC58

C/Species: Neisseria meningitidis

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

C/Accession: G81174

R:Tellet, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.

Science 287, 1809-1815, 2000

A/Authors: Granli, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappunli, R.;

A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A/Reference number: AB1000; MUID:20175755

A/Accession: G81174

A/Status: preliminary

A: Molecule type: DNA
 A: Residues: 1-174 <EXT>
 A: Cross-references: GB:AE002420; GB:AE002098; NID:g7225876; PIDN:AAF41081.1; PID:g722588
 A: Experimental source: serogroup B, strain MC58
 C: Genetics:
 A: Gene: NMB0663

Query Match 94.8%; Score 828.5; DB 2; Length 174;
 Best Local Similarity 96.0%; Pred. No. 2.4e-65;
 Matches 168; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Oy 1 MKKALATIALALPAALAEAGSGFYVQADAAHAKASSISGSAKGFSPRISAGYRINDLR 60
 Db 1 MKKALATIALALPAALAEAGSGFYVQADAAHAKASSISGSAKGFSPRISAGYRINDLR 60
 Oy 61 FAVDYTRKNTKQVPSDFKLYSGASAIYDPDQSPKPYLGLARLSINRASVDNFNSDS 120
 Db 61 FAVDYTRKNTKQVPSDFKLYSGASAIYDPDQSPKPYLGLARLSINRASVDNFNSDS 119
 Oy 121 FSGTSGVLGAGSYAVTPNVLDAGRYNYIGKRVNTKVRSGELSGAVRYKF 175
 Db 120 FSGTSGVLGAGSYAVTPNVLDAGRYNYIGKRVNTKVRSGELSGAVRYKF 174

RESULT 3

opacity protein opaf precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
 N: Alternate names: outer membrane protein opa58
 C: Species: Neisseria gonorrhoeae

A: Variety: strain MS11
 C: Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 26-Aug-1999
 C: Accession: S16611; S36345; S28624
 R: Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, M.; Microbiol. 5, 1889-1901, 1991
 A: Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats
 A: Reference number: S16610; M01D:92114767
 A: Accession: S16611
 A: Molecule type: DNA
 A: Residues: 1-260 <BHA>
 A: Cross-references: EMBL:X52371
 A: Experimental source: strain MS11, variant 4.8
 A: Note: The authors did not translate the sequence for the signal peptide
 A: Note: expression of opacity proteins is regulated by the number of translated repeat
 A: Note: expression of opacity proteins is regulated by the number of translated repeat
 R: Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
 EMO J. 12, 641-650, 1993
 A: Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms of
 A: Reference number: S36328; M01D:93178439
 A: Accession: S36345
 A: Molecule type: DNA
 A: Residues: 24-260 <KUP>
 A: Cross-references: EMBL:Z18937; NID:g49333; PIDN:CAA79370.1; PID:g940799
 A: Experimental source: strain MS11, variant F3
 A: Note: expression of opacity proteins is regulated by the number of translated repeat
 C: Genetics:
 A: Gene: opaf
 C: Superfamily: opacity protein
 C: Keywords: cell surface component; transmembrane protein
 F: 1-10, 11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F: 24-260/Product: opacity protein opaf #status predicted <MAT>
 F: 34-42/Domain: transmembrane #status predicted <TM1>
 F: 34-74/Domain: extracellular #status predicted <EXT1>
 F: 51-60/Region: semivariable region
 F: 51-60/Domain: transmembrane #status predicted <TM2>
 F: 68-94/Domain: transmembrane #status predicted <TM3>
 F: 75-83/Domain: extracellular #status predicted <EXT2>
 F: 85-133/Domain: extracellular #status predicted <EXT2>
 F: 101-128/Region: hypervariable region HV1
 F: 134-148/Domain: transmembrane #status predicted <TM4>
 F: 154-164/Domain: transmembrane #status predicted <TM5>
 F: 165-211/Domain: extracellular #status predicted <EXT3>
 F: 170-217/Region: hypervariable region HV2
 F: 212-224/Domain: transmembrane #status predicted <TM6>

F: 228-236/Domain: transmembrane #status predicted <TM7>
 F: 237-251/Domain: extracellular #status predicted <EXT4>
 F: 252-260/Domain: transmembrane #status predicted <TM8>

Query Match 27.9%; Score 243.5; DB 2; Length 260;
 Best Local Similarity 28.5%; Pred. No. 5.6e-14;
 Matches 73; Conservative 28; Mismatches 72; Indels 83; Gaps 8;

Oy 2 KKALALIALALPAALAEAGSGFYVQADAAHAKASSISGSAKGFSPRISAGYRINDLR 47
 Db 6 KPSLFLSSLLSSAAQAAGDEHGRCPPYQADLAAYETHIDPEQDPSGKISTVSD 65
 Oy 48 -----PRISAGYRINDLRPAVDYTRKNT----- 71
 Db 66 YFRNITRTHIHFRVSVGYPFGGWRIDARRYRKNNNKYSVSIKELLRNKYNRGRTDRK 125
 Oy 72 --KQVPSDFKLYSGASAIYDPDQSPKPYLGLARLSIN--RASVDF----- 115
 Db 126 TENQENGTEHNAVSSLSLAVYDFKLNDRKPYIGARVAAGVHRHSIDSTKTEVTTLH 185
 Oy 116 -----NGSDPSFQTSF-----GLGVLGAGSYAVTPNVLDAGRYNYIGKRVNTV 159
 Db 186 GPGTTPYVPGKNTQDAHRESDSIRRVGLGAVAGVIDITPMLTLDAGRYHYMGRLNWT 245
 Oy 160 KNYRSGELSGAVRYKF 175
 Db 246 R-FKTHASLGVRVF 260

RESULT 4

opacity protein opaf precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

N: Alternate names: outer membrane protein opaf
 C: Species: Neisseria gonorrhoeae
 A: Variety: strain MS11
 C: Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
 C: Accession: S16610
 R: Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc M.; Microbiol. 5, 1889-1901, 1991
 A: Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats
 A: Reference number: S16610; M01D:92114767
 A: Accession: S16610
 A: Molecule type: DNA
 A: Residues: 1-261 <BHA>
 A: Cross-references: EMBL:X52364
 A: Experimental source: strain MS11, variant 4.8
 A: Note: the authors did not translate the sequence for the signal peptide
 A: Note: expression of opacity proteins is regulated by the number of translated repeat
 A: Note: expression of opacity proteins is regulated by the number of translated repeat
 A: Note: expression of opacity proteins is regulated by the number of translated repeat
 C: Genetics:
 A: Gene: opaf
 C: Superfamily: opacity protein
 C: Keywords: cell surface component; transmembrane protein
 F: 1-10, 11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F: 24-261/Product: opacity protein opaf #status predicted <MAT>
 F: 34-42/Domain: transmembrane #status predicted <TM1>
 F: 34-75/Domain: extracellular #status predicted <EXT1>
 F: 51-61/Region: semivariable region
 F: 51-61/Domain: transmembrane #status predicted <TM2>
 F: 76-84/Domain: transmembrane #status predicted <TM3>
 F: 89-95/Domain: extracellular #status predicted <EXT2>
 F: 96-134/Domain: extracellular #status predicted <EXT2>
 F: 109-139/Region: hypervariable region HV1
 F: 138-149/Domain: transmembrane #status predicted <TM4>
 F: 153-165/Domain: transmembrane #status predicted <TM5>
 F: 166-212/Domain: extracellular #status predicted <EXT3>
 F: 171-218/Region: hypervariable region HV2
 F: 213-225/Domain: transmembrane #status predicted <TM6>
 F: 229-237/Domain: transmembrane #status predicted <EXT4>
 F: 238-252/Domain: extracellular #status predicted <EXT4>
 F: 253-261/Domain: transmembrane #status predicted <TM8>

Query Match 27.7%; Score 242; DB 2; Length 261;
 Best Local Similarity 31.0%; Pred. No. 7.6e-14;


```

Oy 116 -----NCSDFSCST----GLGLVLAQVSAVAMPVNDVLDGYRNTIGKAFNEFK 161
Db 166 GTTPYVYGGKNTQDARHRESDSIRRVGLGAVAGVGIDITPNTLIDAGYRHHWGRLENT- 244

Oy 162 VRSGELSGAVRVKF 175
Db 245 FKTHEASLGVRYRF 258

RESULT 7
opacity protein opa57 - Neisseria gonorrhoeae (strain MS11) (fragment)
N/Alternate names: outer membrane protein opa57
C/Species: Neisseria gonorrhoeae
A/Variety: strain MS11
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C/Accession: S36343; S28626
R/Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
EMBO J. 12, 641-650, 1993
A/Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms
A/Reference number: S36343; MUID:93178439
A/Accession: S36343
A/Molecule type: DNA
A/Residues: 1-237 <KUP>
A/Cross-references: EMBL:Z18935; NID:q49331; PIDN:CA479368.1; PID:940797
A/Experimental source: strain MS11, variant F3
A/Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
C/Genetics:
A/Gene: opa57
C/Superfamily: opacity protein
C/Keywords: cell surface component; transmembrane protein
F:1-237/Product: opacity protein opa57 #status predicted <MAT>
F:11-19/Domain: transmembrane #status predicted <TM1>
F:20-51/Domain: extracellular #status predicted <EXT1>
F:28-37/Region: semivariable region
F:52-60/Domain: transmembrane #status predicted <TM2>
F:65-71/Domain: transmembrane #status predicted <TM3>
F:72-110/Domain: extracellular #status predicted <EXT2>
F:78-105/Region: hypervariable region HV1
F:111-125/Domain: transmembrane #status predicted <TM4>
F:131-141/Domain: transmembrane #status predicted <TM5>
F:143-148/Domain: extracellular #status predicted <EXT3>
F:147-154/Region: hypervariable region HV2
F:189-201/Domain: transmembrane #status predicted <TM6>
F:205-213/Domain: transmembrane #status predicted <TM7>
F:214-228/Domain: extracellular #status predicted <EXT4>
F:229-237/Domain: transmembrane #status predicted <TM8>

Query Match 27.5%; Score 240; DB 2; Length 237;
Best Local Similarity 30.3%; Pred. No. 1e-13;
Matches 72; Conservative 26; Mismatches 60; Indels 80; Gaps 9;

Oy 17 ALAEGASFFVQADAAHA-----KASSLSG-----AKGFSPIRISAGY 54
Db 1 ASEDGGRPPYQADALAYVEHTHDYPEPTAPNNKKISTVSDFNIRTSRVHPRVSGY 60

Oy 55 RINDLRFPVADTVTRY---NYKQVPS-----TDFK-----LYSTIAS 87
Db 61 DFGGRRIADADARTRKKMNKKTSVSIKELLRNKNGNFRDILKAENOENGTFHAAVSSDLS 120

Oy 88 AIYDPTOSPPKPYLGARLSLN--RASVDF-----NGSDF 121
Db 121 AVYDRLKMDKRFPIGAVNAGVHSHSDTSKTTTEVTTLILHGPTTPTFYVPGKRTQDAH 180

Oy 122 SQTST----GLGVLAGVSAVATPNVDLDAGTRNTIGKAVNTVKNVRSGLSAGVRYKF 175
Db 181 RESDSIRRVGLGAVAGVGIDITPNTLIDAGYRHHWGRLENT- FKTHEASLGVRYRF 237

RESULT 8
516613
opacity protein opa6 precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

```

C.Species: Neisseria gonorrhoeae
A.Variety: strain MS11
C.Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
Accession: S16613
R.Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Rupsec Mol. Microbiol. 5, 1889-1901, 1991
Article: The opacity proteins of *Neisseria gonorrhoeae* strain MS11 are encoded by a f
A.Reference number: s16610; MUID:92114767
Accession: S16613
Molecule type: DNA
Residues: 1-338 <BHA>
Cross-references: EMBL:X52373
Experimental source: strain MS11, variant 4.8
Note: the authors did not translate the sequence for the signal peptide
of repeats place the start codon in frame with the rest of the protein
Genetics:
AGene: opab
CSuperfamily: Opacity protein
Keywords: Cell surface component; transmembrane protein
F.1-3,14-104/Domains: signal sequence (fragments) #status predicted <SIG>
F.105-338/Product: opacity protein opab #status predicted <MAT>
F.115-123/Domains: transmembrane #status predicted <TM1>
F.115-123/Domains: extracellular #status predicted <EXT1>
F.124-155/Domains: extracellular #status predicted <EXT1>
F.132-141/Region: semi-variable region
F.156-164/Domains: transmembrane #status predicted <TM2>
F.169-175/Domains: transmembrane #status predicted <TM3>
F.176-212/Domains: extracellular #status predicted <EXT2>
F.182-207/Region: hypervariable region HV1
F.213-227/Domains: transmembrane #status predicted <TM4>
F.224-289/Domains: extracellular #status predicted <EXT3>
E.233-243/Domains: transmembrane #status predicted <TM5>
F.249-295/Region: hypervariable region HV2
F.306-310/Domains: transmembrane #status predicted <TM6>
F.306-314/Domains: transmembrane #status predicted <TM7>
F.315-329/Domains: extracellular #status predicted <EXT4>
F.330-338/Domains: transmembrane #status predicted <TM8>

Query Match 27.5%; Score 240; DB 2; Length 338;
Best Local Similarity 28.8%; Pred.No. 1.5e+13;
Matches 70; Conservative 29; Mismatches 66; Indels 78; Gaps 8;

DQ 10 ALALPAALAIEGASGFVQAADAH-----KASSLSGS-----AKGF 46
 ::|||::|||||::|
DB 97 SLFLPAPARASENGSGPYQAADLAETAEERTHDYPEPTGAKKDKSTVDYFRNIRHSI 156
 ::|||::|
DQ 47 SPRIISAGRYINDLRFAVDYTRYKNY-----KQVSDFEKI 81
 ::|||::|
DB 157 HPRVASGVDEFGWMRIAIDYARYRKRMNDKYSVIDIKELNQNKKDLKTENGEHTPAY 216
 ::|||::|
DQ 82 YSISGSAITDYDPQTSPVAFYLIGARLSLN--RASVDF-----N 116
 ::|||::|::|::|::|::|::|
DB 217 SSLGLSSAYIDEFLNKRFPIYGARVAIGHVRSHSIDSTRKTKFKLTSSGYGLNPVTYEEN 276
 ::|||::|::|::|::|::|::|
DQ 117 GSDFSQSOTST---GLGIAGLYAGSVYAATPNVDLDACGRNYNTICKVNTYNVRSSELSAGVR 172
 ::|||::|::|::|::|::|::|
DB 277 TGNNAHQNSIRRVGLGYLAGVGFDITPKLLDTGTGRHYHGRLFNTR-FTHHASLGVR 335
 ::|||::|
DQ 173 VKF 175
 ::|
DB 336 VRF 338

RESULT 9
S20043
opacity protein B precursor (clone pFOB1700) - *Neisseria meningitidis* (strain FAM18)
N.Alternate names: outer membrane protein class 5
C.Species: *Neisseria meningitidis*
A.Variety: strain FAM18
C.Date: 04-Jun-1997 #sequence_revision 04-Jun-1997 #text_change 17-Oct-1997
Accession: S20043
R.Aho, E.L.; Dempsey, J.A.; Hobbs, M.M.; Klapper, D.G.; Cannon, J.G.
Mol. Microbiol. 5, 1429-1437, 1991

A:Title: Characterization of the opa (class 5) gene family of *Neisseria meningitidis*.
 A:Reference number: S16286; MUID:92157869
 A:Accession: S20043
 A:Molecule type: DNA
 A:Residues: 1-254 <AH0>
 A:Cross-references: EMBL:X63108
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
 A:Note: only a part of the translation is shown
 A:Note: expression of opacity proteins is regulated by the number of translated repeat
 C:Genetics:
 A:Gene: opaB
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-19/Domain: signal sequence (fragment) #status predicted <SIG>
 F:20-254/Product: opacity protein opaB #status predicted <MAT>
 F:21-39/Domain: transmembrane #status predicted <TM1>
 F:40-69/Domain: extracellular #status predicted <EXT1>
 F:48-55/Region: semivariable region
 F:70-78/Domain: transmembrane #status predicted <TM2>
 F:83-89/Domain: transmembrane #status predicted <TM3>
 F:90-126/Domain: extracellular #status predicted <EXT2>
 F:96-121/Region: hypervariable region HV1
 F:127-141/Domain: transmembrane #status predicted <TM4>
 F:147-157/Domain: transmembrane #status predicted <TM5>
 F:158-205/Domain: extracellular #status predicted <EXT3>
 F:163-211/Region: hypervariable region HV2
 F:206-218/Domain: transmembrane #status predicted <TM6>
 F:222-230/Domain: transmembrane #status predicted <TM7>
 F:231-245/Domain: extracellular #status predicted <EXT4>
 F:246-254/Domain: transmembrane #status predicted <TM8>

Query Match 27.4%; Score 239.5; DB 2; Length 254;
 Best Local Similarity 28.7%; Pred. No. 1.2e-13;
 Matches 70; Conservative 29; Mismatches 68; Indels 77; Gaps 7;

```

QY 8 LIALPAALAEAGSGFYVOADAAH-----KASSLSGS-----AKGPS 47
DB 12 LPSAAQAASDEGSSRPYVQADLVAERITHYPKATGANNSTVSDYFNRHSH 71
QY 48 PRISAGYRINDLRFAVDYTRYKNY-----KQVSTDFKLY 82
DB 72 PVSAGYDGFDMRIADYASRYKMNKNKYSVTKLEKNKKDKLKENDENGCFPHAS 131
QY 83 SIGASIVDFEDQSPVKPYLGARLSN--RASVD-----FNQS 118
DB 132 SIGLSAIIIDFKINDKFKPYIGARVAVGHVRRHSIDSTKRTTEVVTLTGADPTKPTIYNGE 191
QY 119 -----DSFSQSTGLGVLAGVSAVTPNVLDAGYRYNYIGKVNIVKNGRSGELSGY 171
DB 192 STQNAVHSHSIRRLGLGVAVAGVDFITPKLITDGYRYHNMGRLENTFR-KTTHVSLSGM 250
QY 172 RYKF 175
DB 251 RYHF 254

```

RESULT 10
 S16614
 opacity protein opaF precursor - *Neisseria gonorrhoeae* (strain MS11) (fragments)
 C:Species: *Neisseria gonorrhoeae*
 A:Variety: strain MS11
 C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
 C:Accession: S16614
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, M.O. Microbiol. 5, 1689-1901, 1991
 A:Title: The opacity proteins of *Neisseria gonorrhoeae* strain MS11 are encoded by a family
 A:Reference number: S16610; MUID:92114767
 A:Molecule type: DNA
 A:Residues: 1-257 <BHA>
 A:Cross-references: EMBL:X52368

A:Experimental source: strain MS11, variant 4.8
 A:Note: the authors translated the codon ACC for residue 206 as Ala and TAT for resid
 A:Note: the authors did not translate the sequence for the signal peptide
 A:Note: expression of opacity proteins is regulated by the number of translated repea
 C:Genetics:
 A:Gene: opaF
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10/11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-257/Product: opacity protein opaF #status predicted <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-74/Domain: extracellular #status predicted <EXT1>
 F:51-60/Region: semivariable region
 F:75-80/Domain: transmembrane #status predicted <TM2>
 F:88-94/Domain: transmembrane #status predicted <TM3>
 F:95-131/Domain: extracellular #status predicted <EXT2>
 F:101-126/Region: hypervariable region HV1
 F:132-146/Domain: transmembrane #status predicted <TM4>
 F:152-162/Domain: transmembrane #status predicted <TM5>
 F:163-208/Domain: extracellular #status predicted <EXT3>
 F:168-214/Region: hypervariable region HV2
 F:209-221/Domain: transmembrane #status predicted <TM6>
 F:225-233/Domain: transmembrane #status predicted <TM7>
 F:234-248/Domain: extracellular #status predicted <EXT4>
 F:249-257/Domain: transmembrane #status predicted <TM8>

Query Match 27.38%; Score 239; DB 2; Length 257;
 Best Local Similarity 28.1%; Pred. No. 1.4e-13;
 Matches 71; Conservative 30; Mismatches 72; Indels 80; Gaps 8;

```

QY 2 KKALALIALPAALAEAGSGFYVOADAAH-----KASSLSGS-----AKGPS 44
DB 6 KKPILLSLSLSSAQAASDEGSSRPYVQADLVAERITHYPEPTGKKKISTVSD 65
QY 45 -----GSPRISAGYRINDLRFAVDYTRYKNY-----KQVSTDFKLY 82
DB 66 YFNIRTHSHIPRVSVGYDFGGMRIADYARYKMNKNKYSVTKLEKNKKDKLKENDENGCFPHAS 131
QY 72 KQVSTDFKLYSIGASIVDFEDQSPVKPYLGARLSN--RASVD-----FNQS 118
DB 126 NQENGTHAVSSIGLSAIIIDFKINDKFKPYIGARVAVGHVRRHSIDSTKRTTEVVTLTGADPTKPTIYNGE 191
QY 116 -----NCSFSQSTGLGVLAGVSAVTPNVLDAGYRYNYIGKVNIVKNGRSGELSGY 171
DB 186 LNPTVTEENTQNAHNSIRRLGLGVAVAGVDFITPKLITDGYRYHNMGRLENTFR-F 244
QY 163 RSGELSGYRYKF 175
DB 245 KTHRASLSGVRHYRF 257

```

RESULT 11
 KONH2C
 opacity protein P.IIC precursor - *Neisseria gonorrhoeae* (strain JS3) (fragments)
 N:Alternate names: outer membrane protein P.IIC
 C:Species: *Neisseria gonorrhoeae*
 A:Variety: strain JS3
 C:Date: 31-Mar-1992 #sequence_revision 17-Oct-1997 #text_change 08-May-1998
 C:Accession: S03095; S16360
 R:van der Ley, P.
 M.O. Microbiol. 2, 797-806, 1988
 A:Title: Three copies of a single protein II-encoding sequence in the genome of *Neiss*
 A:Reference number: S03095; MUID:89096501
 A:Accession: S03095
 A:Molecule type: DNA
 A:Residues: 1-268 <VAN>
 A:Cross-references: EMBL:X12625
 A:Experimental source: strain JS3
 A:Note: 241-Val was also found
 A:Note: expression of opacity proteins is regulated by the number of translated repea
 C:Genetics:
 A:Gene: opaF
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10/11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-257/Product: opacity protein opaF #status predicted <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-74/Domain: extracellular #status predicted <EXT1>
 F:51-60/Region: semivariable region
 F:75-80/Domain: transmembrane #status predicted <TM2>
 F:88-94/Domain: transmembrane #status predicted <TM3>
 F:95-131/Domain: extracellular #status predicted <EXT2>
 F:101-126/Region: hypervariable region HV1
 F:132-146/Domain: transmembrane #status predicted <TM4>
 F:152-162/Domain: transmembrane #status predicted <TM5>
 F:163-208/Domain: extracellular #status predicted <EXT3>
 F:168-214/Region: hypervariable region HV2
 F:209-221/Domain: transmembrane #status predicted <TM6>
 F:225-233/Domain: transmembrane #status predicted <TM7>
 F:234-248/Domain: extracellular #status predicted <EXT4>
 F:249-257/Domain: transmembrane #status predicted <TM8>

EMBO J. 12, 641-650, 1993

A:Title: Variable opacity (opa) outer membrane proteins account for the cell tropisms of

A:Reference number: S36328; MUID:93178439

A:Accession: S36328

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 25-260 <KUP>

A:Cross-references: EMBL:Z18927; NID:949323; PIDN:CAA79360.1; PID:9440789

R: Meyer, T.P.

submitted to the EMBL Data Library, November 1992

A:Reference number: S28617

A:Accession: S28621

A:Molecule type: DNA

A:Residues: 25-260 <MEY>

A:Cross-references: EMBL:Z18927; NID:949323; PIDN:CAA79360.1; PID:9440789

C:Genetics:

A:Gene: opa

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-11,12-24/Domain: signal sequence (fragments) #status predicted <SIG>

F:25-260/Product: opacity protein opa #status predicted <MAT>

F:35-43/Domain: transmembrane #status predicted <TM1>

F:44-75/Domain: extracellular #status predicted <EXT1>

F:52-61/Domain: semivariable region

F:76-84/Domain: transmembrane #status predicted <TM2>

F:89-95/Domain: transmembrane #status predicted <TM3>

F:96-134/Domain: extracellular #status predicted <EXT2>

F:102-129/Region: hypervariable region HV1

F:135-149/Domain: transmembrane #status predicted <TM4>

F:155-165/Domain: transmembrane #status predicted <TM5>

F:166-211/Domain: extracellular #status predicted <EXT3>

F:11-217/Region: hypervariable region HV2

F:212-224/Domain: transmembrane #status predicted <TM6>

F:228-236/Domain: transmembrane #status predicted <TM7>

F:237-251/Domain: extracellular #status predicted <EXT4>

F:252-260/Domain: transmembrane #status predicted <TM8>

Query Match

Best Local Similarity 27.2%; Score 237.5; DB 1; Length 260;

Matches 73; Conservative 26; Mismatches 68; Indels 83; Gaps 8;

QY	6	AAIATAALPAAALAGASGYOADAHA-----KASSISGSAKGS-----	47
DB	14	SSILFSSAQAQASDEGGRGYOADAHAHEITHDYPKPTPSKGIKSTVSDYPRNIRT	73

QY	48	-----PRISAGYRINDLRFADVTRY-----KNK-----QYPS	76
DB	74	HSIHPRVSYGYDEGGRRIADYARAKMSDNKYSIKMRVHKHNSRKNLKTENDENG	133

QY	77	TDFKLSTIGASATYDDTQSPYKPYLGARLSIN--RASVD-----	114
DB	134	SFHAASLSLSATYDQINDKRPYIGARVAVGHRHSIDSTKLTGLLTSTPGIMSGV	193

QY	115	-----FNGSDSFQSTSTGLVAGSYAVPNVDLACGYRNTYGNKYNKVRBSG	165
DB	194	YKVLRTPGAHRESDSIR--VGLGYIAGVGPDITPKLTLDGGRHNMGRLENT--FKTH	250

QY	166	ELISAGYRAVF	175
DB	251	EASLGYRRAVF	260

RESULT 14

S16616

opacity protein opa precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

C:Species: Neisseria gonorrhoeae

A:Variety: strain MS11

C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997

C:Accession: S16616

R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch,

Mol. Microbiol. 5, 1989-1990, 1991

A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam

A:Reference number: S16610; MUID:92114767

A:Accession: S16616

A:Molecule type: DNA

A:Residues: 1-266 <BHA>

A:Cross-references: EMBL:X52372

A:Experimental source: strain MS11, variant 4.8

A>Note: the authors did not translate the sequence for the signal peptide

of repeats place the start codon in frame with the rest of the protein

C:Genetics:

A:Gene: opa

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>

F:24-266/Product: opacity protein opa #status predicted <MAT>

F:34-42/Domain: transmembrane #status predicted <TM1>

F:43-74/Domain: extracellular #status predicted <EXT1>

F:51-60/Region: semivariable region

F:75-83/Domain: transmembrane #status predicted <TM2>

F:88-94/Domain: transmembrane #status predicted <TM3>

F:95-139/Domain: extracellular #status predicted <EXT2>

F:101-134/Region: hypervariable region HV1

F:140-154/Domain: transmembrane #status predicted <TM4>

F:160-170/Domain: transmembrane #status predicted <TM5>

F:171-217/Domain: extracellular #status predicted <EXT3>

F:176-223/Region: hypervariable region HV2

F:218-230/Domain: transmembrane #status predicted <TM6>

F:234-242/Domain: transmembrane #status predicted <TM7>

F:243-257/Domain: extracellular #status predicted <EXT4>

F:258-266/Domain: transmembrane #status predicted <TM8>

Query Match

Best Local Similarity 27.2%; Score 237.5; DB 2; Length 266;

Matches 76; Conservative 25; Mismatches 72; Indels 89; Gaps 8;

QY	2	KKALAAIALPAAALAGS---ASGEYVQADAHA-----KASSISGS-	42
DB	6	KPSLSSLSFSSAQAQAGEHGRGYOADAHAHEITHDYPEQYAPKKAQLSYSD	65

QY	43	-----AKGSPRISAGYRINDLRFADVTRYK-----NYQVSTP-	78
DB	66	YFNIRTHSHIPRVSYGYDEGGRRIADYARAKMSDNKYSIKMRVHKHNSRKNLKTENDENG	125

QY	79	-----FKLSTIGASATYDDTQSPYKPYLGARLSIN--RASVD-----	110
DB	126	NIKTRTEHRENGTFRHAASLSLAVDEDTGSRKPYIGARVAVGHRHNSRKNLKTENDENG	185

QY	111	-----ASVDFNG-----SDSFQSTSTGLVAGSYAVPNVDLACGYRNTYGNKYNKVRBSG	165
DB	186	AVTTYQNAASVTYNAPRKLPHEHSRSLSGAVAGVIDITPMLTLDAGRYHNM	245

QY	154	GKYNVKNVRSGLSAGYRAVF	175
DB	246	GRLENT--FKTHEASLGYRAVF	266

RESULT 15

F64124

opacity protein homolog H1457 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999

C:Accession: F64124

R:Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage

; D.M.; Brannon, J.; Scott, J.; Shirley, R.; Liu, L.T.; Glodok, A.; Kelley, J.M.; Weidman

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630

C:Accession: F64124

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-178 <TIGR>

A:Cross-references: GB:U32823; GB:U42023; NID:91574281; PIDN:AAC23104.1; PID:91574294

Tue Oct 29 09:23:14 2002

us-09-684-883-4.rpr

Page 8

Query Match	27.1%	Score 236.5;	DB 2;	Length 178;
Best Local Similarity	35.4%;	Prod. No. 1.5e-13;		
Matches	68;	Conservative	24;	Mismatches 65;
			Indels	31;
			Gaps	9

```

QY      1 MKKALLAALATLALPAALAAEAGSAFYYOA-----DAHAAKSSLSLAKGSPKRIASG 35
Db      1 MKKALLVYMLFPLALSAQAQ-----WYQGGDLGASKIDITHVSSNS-----PSFQRIISVG 52

QY      54 YRIN-DLRFAYVDYTRY-----KNYQVPSDTPFKLYSIGSASAIYDEPTQSPWPKYGLAETSL 108
        | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      53 YARDKRFRLAYDYTRYNGYVYANTADVVDVSLKKSSLGTLGFGFDPL-ADFEPYGVAVST 111

QY      109 NRKASVDENG-----DSF--SQTSGTGLVLAGVSAATVPNTDLAGRYNYTIKVTIVKVR 163
        | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      112 NGADVYANARYRIETEFNTEFRIGALAGVQIKLDINALNTNIETVRL-----AASNV 166

QY      164 SGELSGAVRYKF 175
        : | | : | |
Db      167 DVGKAGLRPSF 178

```

Search completed: October 28, 2002, 16:03:35
Job time : 13.5538 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:55:44 ; Search time 7.03013 Seconds

(without alignments)
963.840 Million cell updates/sec

Title: US-09-684-883-4

Perfect score: 874
Sequence: 1 MKKALALALALPALALAE.....VNTYKNVSGELSGACRVK 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	240	27.5	237	1 OPAK_NEIGO	Q04880 neisseria g
2	239	27.3	270	1 OMPC_NEIGO	P09888 neisseria g
3	238.5	27.3	233	1 OPE7_NEIGO	O05034 neisseria g
4	236.5	27.1	178	1 VES7_HAEN	O57201 haemophilus
5	234.5	26.8	238	1 OPAH_NEIGO	Q04884 neisseria g
6	234	26.8	237	1 OPAJ_NEIGO	Q04882 neisseria g
7	231.5	26.5	236	1 OPAC_NEIGO	P11296 neisseria g
8	231	26.4	234	1 OPAB_NEIGO	Q04874 neisseria g
9	230.5	26.4	234	1 OPAE_NEIGO	Q04878 neisseria g
10	230.5	26.4	234	1 OPAF_NEIGO	Q04878 neisseria g
11	229.5	26.3	238	1 OPE6_NEIGO	O05033 neisseria g
12	227.5	26.0	260	1 OPR1_NEIMC	P10170 neisseria m
13	224.5	25.7	234	1 OPE2_NEIGO	P11297 neisseria g
14	224.5	25.7	234	1 OPE5_NEIGO	Q04885 neisseria g
15	223	25.5	243	1 OPAD_NEIGO	Q04883 neisseria g
16	222.5	25.5	238	1 OPE8_NEIGO	Q04881 neisseria g
17	222.5	25.5	244	1 OPAI_NEIGO	Q04877 neisseria g
18	210.5	24.1	239	1 OPAI_NEIGO	Q04876 neisseria g
19	208	23.8	247	1 OPAG_NEIGO	Q04875 neisseria g
20	181	20.7	121	1 OPA_HAEN	P45088 haemophilus
21	138.5	15.8	170	1 OPR3_NEIMC	P10171 neisseria m
22	122.5	14.0	70	1 Y414_HAEN	O57392 haemophilus
23	108.5	12.4	182	1 AIL_YERPS	Q56957 yersinia ps
24	103.5	11.8	353	1 OM52_HAEN	P38366 haemophilus
25	100.5	11.5	213	1 OM25_BRUAB	Q44664 brucella ab
26	96.5	11.0	178	1 AIL_YEREN	P16454 yersinia en
27	95.5	10.9	212	1 OMPW_ECOLI	P21364 escherichia
28	94.5	10.8	213	1 OM25_BRUSU	Q45689 brucella su
29	94.5	10.8	521	1 TSAS_RICIS	P37917 rickettsia
30	93.5	10.7	350	1 PORF_PSEAE	P13794 pseudomonas
31	93.5	10.7	353	1 OM51_HAEN	P43840 haemophilus
32	93.5	10.7	359	1 OM53_HAEN	P45966 haemophilus
33	93	10.6	350	1 OMPA_SALTY	P02936 salmonella

34	92.5	10.6	213	1 OM25_BRUME	Q45321 brucella me
35	92.5	10.6	349	1 OMPA_BUCAI	P57414 buchnera ap
36	90	10.3	428	1 OM47_PASMT	P80603 pasteurella
37	89	10.2	993	1 Y109_YEAST	P40442 saccharomyc
38	88.5	10.1	201	1 OM25_BRUOV	O45335 brucella oy
39	87	10.0	325	1 MODD_MYCRO	O30620 mycobacteri
40	86.5	9.9	213	1 OM25_BRUCA	O45110 mycobacteri
41	86.5	9.9	213	1 OM25_BRUNE	O45110 mycobacteri
42	86	9.8	282	1 MSP4_ANAMA	Q07408 anaplasm
43	86	9.8	325	1 MODD_MYCTU	O50906 mycobacteri
44	85.5	9.8	376	1 OMPC_SERMA	O54471 serratia ma
45	83	9.5	240	1 OM31_BRUME	Q45322 brucella me

ALIGNMENTS

RESULT 1	OPAK_NEIGO	STANDARD;	PRT;	237 AA.
ID	OPAK_NEIGO			
AC	Q04880;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	01-NOV-1995 (Rel. 32, Last annotation update)			
DE	Opacity Protein OPA57 precursor (Fragment).			
GN	OPAK.			
OS	Neisseria gonorrhoeae.			
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			
OX	NCBI_TaxID:485;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MS11 / F3;			
RX	MDLINE=93178439; PubMed=8440254;			
RA	Kirsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;			
RT	"Variable opacity (Opa) outer membrane proteins account for the cell			
RT	tropisms displayed by Neisseria gonorrhoeae for human leukocytes and			
RT	epithelial cells.";			
RL	EMBO J. 12:641-650(1993).			
CC	-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA			
CC	PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE			
CC	VARIATION.			
CC	-1- SUBCELLULAR LOCATION: Outer membrane.			
CC	-1- This SWISS-PROT entry is copyright. It is produced through a collaboration			
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DR	EMBL; Z18935; CAAT9368.1; -			
DR	PIR; S28626; S28626.			
DR	InterPro; IPR003394; Opacity.			
DR	Pfam; PF02462; Opacity; 1.			
KW	Outer membrane; Multigene family; Signal.			
FT	NON_TER	1		
FT	SIGNAL	<1		
FT	CHAIN	2	>237	POTENTIAL.
FT	NON_TER	237		OPACITY PROTEIN OPA57.
SQ	SEQUENCE	237 AA;	26703 MW;	F8B1A0FB5C7EBGAD CRC64;
Query Match		27.5%;	Score 240;	DB 1; Length 237;
Best local similarity		30.3%;	Pred. No. 2.9e-14;	
Matches	72;	Conservative	26;	Mismatches 60; Indels 80; Gaps 9;
OY	17 ALAGAGAGFYQADAAHA-----KASSISLGS-----AKGSPRISAGY 54			
DB	1 ASEGEGGPGYQADLAVAYEHITHDYPEAPNPKNKISTVSDYFRNIRFSVHPRVSVGY 60			
OY	55 RINDLRAVAVYTRYK---NTRKQVPS-----TDFK-----LYSIGAS 87			
DB	61 DFGGRIADYARIKRNKNNKYSISIKELLRNKNGNKGRTDLKAEQNBNGTFHAAVSLGLS 120			


```

Oy 88 AYDDPQSPVRYGARLSLN- -RASDF-----NGSOF 121
Db 121 AYIDKLDKRRKPYIGARVAYGVHSHSIDSTKKTTEVTTLIHGPOTPPYVPGKTKQDAN 180
Oy 122 SQTST-----GLGLVLAGVSAYATPVNVDLDGACRYNICKGVNFKVNRSGELASGVKRF 175
Db 181 RESDSIRRVGICGAVAGVGDITPNTLTIDAGYRYHYHWGRLENR- KPTHASLGVRYRF 237

RESULT 2
OMPC_NEIGO STANDARD: PRT; 270 AA.
AC P09888;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Outer membrane protein P.IIC precursor (Protein IIC).
GN PIIC.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J53;
RX MEDLINE=89096501; PubMed=3145386;
RA van der Ley P.;
RT "Three copies of a single protein II-encoding sequence in the genome
RT of Neisseria gonorrhoeae J53: evidence for gene conversion and gene
RT duplication."
RT Mol. Microbiol. 2:797-806(1988).
CC -1- FUNCTION: THIS PROTEIN SERVES AS A PORIN.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; X12625; CAA31144.1; -.
DR PIR; S03095; KONH2C.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity: 1.
KW Outer membrane; Porin; Transmembrane; Antigen; Signal.
FT SIGNAL 1 25
FT CHAIN 26 270
FT TRANSMEM 36 44 OUTER MEMBRANE PROTEIN P.IIC.
FT TRANSMEM 77 85 POTENTIAL.
FT TRANSMEM 90 96 POTENTIAL.
FT TRANSMEM 143 157 POTENTIAL.
FT TRANSMEM 163 173 POTENTIAL.
FT TRANSMEM 222 234 POTENTIAL.
FT TRANSMEM 238 246 POTENTIAL.
FT TRANSMEM 262 270 POTENTIAL.
SQ SEQUENCE 270 AA; 30269 MW; F6B44837830A50D CRC64;

Query Match 27.3%; Score 239; DB 1; Length 270;
Best Local Similarity 27.2%; Pred. Mismatches 70; Indels 88; Gaps 7;
Matches 70; Conservative 29;

Oy 6 AALLIALPAAALAGSAGFYQADAAIAKA-----SSSLGSAK----- 44
Db 15 SLLFSSAARAASSEGGSGPYQADLAAYAAERITTHDYPRPTGTGNKISTVSDYFRNIRT 74
Oy 45 -GFSPRIAGYRINDLFAVDYTRKNNK----- 72
Db 75 HSYHFRVAVGVDFGSMRIADYARKRKNNNNKYSVSTIKELLRNDNSAGSVGRHNLITQTK 134
Oy 73 ---QVPSIDFKLYISIGASAIYDFDTQSPVRYGARLSINRA-----SVD----- 114

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Db 125 TEHQNGNEFFHVAVSSIGLSTIVDFDGSNRPKPIGNRAVAGHNRHQVRSVEDETEIITTP 194
OY 115 FNGSDSFSCOTS-----TGLGVLAGVSTAATPENVDDLDAGRYNYTKYNT 158
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 195 SNGGCKVSSGKSMKPKSAHSHNSIRRVGLGVLAGVGFEDITPILTDGRYHNMGRLEN 254
OY 159 VKNVRSGLSAGSVRYKF 175
    :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 255 TR-FTTHEASLGMRYKF 270

RESULT 3
OP67_NEIGO
ID OP67_NEIGO STANDARD: PRT: 233 AA.
AC 005034;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA67 precursor (Fragment).
OC Neisseria gonorrhoeae
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI;
RX MEDLINE=931176439; PubMed=8440254;
RA Kupsch E. M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells.";
RL EMBL J. 12:641-650(1993).
CC -! FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -! SUBCELLULAR LOCATION: Outer membrane.
CC CC
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CC CC
CC DR EMBL: Z18942; CAA79375.1; -.
CC DR PIR: S28625; S28625.
CC DR InterPro: IPR003594; Opacity.
CC DR Pfam: PF02462; Opacity; 1.
CC KW Outer membrane; Multigene family; Signal.
CC FT SIGNAL 1 1
CC FT CHAIN 2 >233 POTENTIAL.
CC FT NON_TER 233 233 OPACITY PROTEIN OPA67.
CC SQ SEQUENCE 233 AA; 26039 MW; 6C13A46AB163C67F CRC64;

Query Match 27.3%; Score 238.5; DB 1: Length 233;
Best Local Similarity 26.3%; Pred. 3.8e-14;
Matches 66; Conservative 32; Mismatches 58; Indels 77; Gaps 8;

OY 19 AEG-ASGEVVOADAHA-----KASSLSGAKGF-----SPRISAGY 54
    :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2 SEGNGRGPVYQDLAAVIAERITHDYPEADQKKGTTSVSDYFNNITHSVHPRVSIGY 61
OY 55 RINDRFPAVDITRRKYNY-----KQVPSTDFKLYSIGASAIYFD 93
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 62 DFGWRIRADYARVYRKMNNSKYSIKKLQNYNKKTEOENGTFHAASLIGLSAVYDFK 121
OY 94 TQSPKPTLGAALSLN--RASVDF-----NGSDSFSCOTS 126
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 122 LNDKRPPIYGARVAGYHRHSIDSTKTKTTGFLTITGAGAGAAPTYSSPKNTDADAQESNS 181
OY 127 ---GLGVLAGVSTAATPENVDDLDAGRYNYTKYNTVKNVRSGLSAGVRYKF 175

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1000

100

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OY 17 ALAAGAGGFPYQAOAAAH-----KASSLSG-----AKFSPRIAGY 54
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 ASEDGGKFPYQADLATAVEHITHDYEPPTAPNKKISTYSDYRNIRTRBSYHRRVGV 60
OY 55 RINDLRFAVDYTRYKNY-----KQVSTDEKLYSTGAS 87
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 DFGGMRTAADYARYRKMMNNKSYNIENVRIRKENGIRIDRKTEOENGCFHAAVSLGLS 120
OY 88 AIYGFDDQSPKPKYLGARSLN--RASVDF-----N 116
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 AIYFOINDKKRPYIGARVAIGHYRHSIDSKRTILEYTVTSNAPNCAVTTYNTPDKTON 180
OY 117 GDSFESQTSGLGYAGSYAVTPNVDIAGYRYNYIGKVTYKNVNSGEISAGYRKF 175
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 DYQNSISIRVGLIAGYAGFDITPKLTIDAGYRYHNMGRLENTFR-FKTHEASLGVRKF 238

RESULT 6
OPAJ_NEIGO          STANDARD;          PRT;          237 AA.
AC      Q04882;
DT      01-OCT-1993 (Rel. 27, Created)
DT      01-OCT-1993 (Rel. 27, Last sequence update)
DT      01-NOV-1995 (Rel. 32, Last annotation update)
DE      Opacity protein OPA58 precursor (Fragment).
GN      OPAJ.
OS      Neisseria gonorrhoeae.
OC      Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX      NCBI_TaxID=485;
      ||
RP      SEQUENCE FROM N.A.
RC      MEDLINE=931178439; PubMed=8440254;
RA      Kusch E.-W., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT      "Variable opacity (Opa) outer membrane proteins account for the cell
RT      tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT      epithelial cells.";
RL      EMBO J. 12:641-650(1993).
CC      -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC      PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC      VARIATION.
CC      -1- SUBCELLULAR LOCATION: Outer membrane.
CC
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CC      or send an email to license@sib-sib.ch).
CC
CC      EMBL; Z18937; CAA79370.1; -.
DR      EMBL; S28624; S28624.
DR      InterPro; IPR003394; Opacity.
DR      Pfam; PF02462; Opacity; 1.
KW      Outer membrane; Multigene family; Signal.
FT      NON_TER          1
FT      SIGNAL          1
FT      CHAIN           2 >237          POTENTIAL.
FT      NON_TER          237          OPACITY PROTEIN OPA58.
SQ      SEQUENCE      237 AA; 26855 MW; B165033B2CDB6A53 CRC64;

Query Match          26.8%; Score 234; DB 1; Length 237;
Best Local Similarity 28.6%; Pred. No. 9,6e-14;
Matches 66; Conservative 26; Mismatches 59; Indels .80; Gaps
OY 24 GFFVQADAHA-----KASSISGSAKGSF-----PRISAGYRINDLRF 61
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8 GFFVQADALAAVEHITHDYPEQTDPSKGIYSVDFRNIRTHSHIPRVSYGDFGGMRI 67
OY 62 AVDYIRKYNY-----KQVSTDEKLYSIGASAIYDEPT 94
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db      68 AADYARRKWNNNKYSVSIKEILLNKYNNGNTDRKTENQNGTTHAIVSLGSAVDPEKL 127
Oy      95 QSPVKPTLIGANLSLN--RASDF-----NGDSFSGOTSF-- 126
Dn      128 NDNRKPPIGAHVAAAGHVKHSIDSTRKTEVTTLIHGPETPTPYPGKNFTODAHRESOSIR 187
Oy      127 --GGCVLAGVSAYTPNVYDLTAGRYNATYGKVNTVKNVSCGLSAGYRVKF 175
Dn      188 RVGLGNVAVGVIDITPNTLTLDAGRHYHWGRLEMT-R-EKTHEASLGAVXRF 237

RESULT 7
OPAC_NEIGO OPAC_NEIGO STANDARD; PRT; 236 AA.
AC          P11296;
DT          01-JUL-1989 (Rel. 11, Created)
DT          01-JUL-1989 (Rel. 11, Last sequence update)
DT          01-NOV-1995 (Rel. 32, Last annotation update)
DE          Opacity protein OPA50 precursor (OPA30) (VO) (Fragment).
GN          OPAC.
OS          Neisseria gonorrhoeae.
OC          Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
CX          NCBI_TaxID=485;
RN          [1]
RP          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC          STRAIN=M51 / VO;
RX          MEDLINE=87002493; PubMed=3093085;
RA          Stern A., Brown M., Nickel P., Meyer T.F.;
RT          "Opacity genes in Neisseria gonorrhoeae: control of phase and antigenic variation."; Cell 47:61-71(1986).
RL          [2]
RN          SEQUENCE FROM N.A.
RP          STRAIN=M51 / F3;
RX          MEDLINE=93178439; PubMed=8440254;
RA          Kusch E.-M., Knappert B., Kuraki T., Heuer I., Meyer T.F.;
RT          "Variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells."; EMBO J. 12:641-650(1993).
CC          -1- FUNCTION: IS IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE VARIATION.
CC          -1- SUBCELLULAR LOCATION: Outer membrane.
CC          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch).
CC          -----
CC          EMBL; M14746; -, NOT_ANNOTATED_CDS.
DR          EMBL; Z18927; CAA79360.1; -.
DR          PIR; A24429; KONHO.
DR          PIR; S28621; S28621.
DR          PIR; S36328; S36328.
DR          InterPro: IPRO03394; Opacity.
DR          Pfam: PF02462; Opacity; 1.
KW          Outer membrane; Multigene family; Signal.
FT          SIGNAL              1
FT          NON_TER            1
FT          CHAIN               2 >236 POTENTIAL.
FT          NON_TER            236    OPACITY PROTEIN OPA50.
SQ          SEQUENCE   236 AA; 26685 MW; 6BDC2C37692183398 CRC64;

Query Match          26.5%; Score 231.5; DB 1; Length 236;
Best Local Similarity 29.7%; Pred. No. 1,6e-13;
Matches       71; Conservative 22; Mismatches 63; Indels 83; Gaps 8

17 ALAEAGSGGYVDAADHA-----KASSLSGAKGFS-----PRISAGY 54
| : | | | | | | | : | | | | | | | | | | | | | | | | | | |

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Db 1 ASDEGGRGVQADLAAYEHITHDYPKPTDPSKGIISTVDFRNIRHSHIPRVSVG 60
 QY 55 RINDLRADVTRY-----KNYK---QVPTDFKLISGAS 87
 Db 61 DFGWRIADYARVARKWDSNKYSVSIKNNMVKHNSNRKRLKTENQENSGFAVSSLGIS 120
 QY 88 AIYDFDQSPVKPYLGRSLN--RASVD-----FN 116
 Db 121 AIYDFQINDKFKPYIGARVAVGVRHSIDSTKKTIGLTTPSPGINSGVYKVLRTPGAHR 180
 QY 117 GSDSFQSTGTGLGVAVSVAVPNDLDAGYRNYIGKRVNYSGELISAGVYK 175
 Db 181 ESDSIR--VGLGVINGVGDITPKLTLDDAGYRHYHMGRLNTR-FKTHASLGAVYRF 236

RESULT 8

OPAB_NEIGO STANDARD; PRT: 234 AA.
 AC 004874;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA51 precursor (Fragment).
 GN OPAB.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 epithelial cells."
 RL EMO J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC
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 CC
 CC EMBL; Z18928; CAA79361.1; -
 DR PIR; S28628; S28628.
 DR PIR; S36329; S36329.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1
 FT CHAIN 2 >234
 FT NON_TER 234 234
 FT CHAIN 234 234
 FT NON_TER 234 234
 SQ SEQUENCE 234 AA; 26772 MW; 9FEEB5DABBA96CA CRC64;

Query Match 26.4%; Score 231; DB 1; Length 234;
 Best Local Similarity 28.2%; Pred. No. 1.7e-13;
 Matches 66; Conservative 29; Mismatches 61; Indels 78; Gaps 8;

QY 19 AEG-ASGVYQADAAHA-----KASSSLGSAK-----GFSPRISAGYR 55
 Db 2 SGNNGRGVYQADLAAYEHITHDYPQGTGKKISTVDFRNIRHSHIPRVSVG 61
 QY 56 INDLRPAVDYTRYKYN-----KQVPTDFKLISGASAIY 90
 Db 62 FGGWRIADYARVARKWDSNKYSVDIKELNKNOKRDLKTENQENSGFAVSSLGISAVY 121

QY 91 DEDTQSPVKPYLGRSLN--RASVD-----NGDSFSQTS 125
 Db 122 DFKLNGKFKRPYIGARVAVGVRHSIDSTKKTTPKLTSSYGLNPPVTEENTQNAHOSN 181
 QY 126 T-----GLGVLAGVSVAVPNDLDAGYRNYIGKRVNYSGELISAGVYK 175
 Db 182 SIRRYGLGVAGVGFDTPKLTLDDAGYRHYHMGRLNTR-FKTHASLGAVYRF 234

RESULT 9

OPAB_NEIGO STANDARD; PRT: 234 AA.
 AC 004878;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA55 precursor (Fragment).
 GN OPAB.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 epithelial cells."
 RL EMO J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC
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 CC
 CC EMBL; Z18933; CAA79366.1; -
 DR PIR; S28632; S28632.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1
 FT CHAIN 2 >234
 FT NON_TER 234 234
 FT CHAIN 234 234
 FT NON_TER 234 234
 SQ SEQUENCE 234 AA; 26881 MW; 8EBB30B3A774C766 CRC64;

Query Match 26.4%; Score 230.5; DB 1; Length 234;
 Best Local Similarity 28.1%; Pred. No. 1.9e-13;
 Matches 64; Conservative 28; Mismatches 59; Indels 77; Gaps 7;

QY 24 GFVYQADAAHA-----KASSSLGSAK-----GFSPRISAGYRINDLAF 61
 Db 8 GFVYQADLAAYEHITHDYPQGTGKKISTVDFRNIRHSHIPRVSVGDFGGMRI 67
 QY 62 AVDTTRYKNT-----KQVPTDFKLISGASAIYDFDTQS 96
 Db 68 AADYARVARKWDSNKYSVDIKELNKNOKRDLKTENQENSGFAVSSLGISAVYDFDKLND 127
 QY 97 PVKPYLGRSLN--RASVD-----KSDSFQSTST---G 127
 Db 128 KFKPYIGARVAVGVRHSIDSTKKTTPKLTSSYGLNPPVTEENTQNAHOSNSIRVG 187
 QY 128 LGVLAGVSVAVPNDLDAGYRNYIGKRVNYSGELISAGVYK 175
 Db 188 LGVLAGVGFDTPKLTLDDAGYRHYHMGRLNTR-FKTHASLGAVYRF 234

RP SEQUENCE FROM N.A.
 RC STRAIN-C1938 / SEROGROUP C;
 RX MEDLINE-88250884; PubMed-2455211;
 RA Stern A., Meyer T.F.;
 RT "Common mechanism controlling phase and antigenic variation in
 pathogenic neisseriae."
 RL Mol. Microbiol. 1:5-12(1987).
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -1- SIMILARITY: STRONG TO THE OPACITY-RELATED PROTEIN POPM3 AND
 CC REGIONS OF HOMOLOG WITH N. GONORRHOEA (STRAIN MS11) OPA GENE
 CC PRODUCTS.
 CC -----
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 CC -----
 DR EMBL; X06445; CAA29748.1; ALT_SEQ.
 DR PIR; S08514; S08514.
 DR InterPro: IPR003394; Opacity.
 DR Pfam; PF02462; Opacity; 1.
 KW Outer membrane.
 SQ SEQUENCE 260 AA; 28936 MW; E847A2843B3F037B CRC64;
 Query Match 26.0%; Score 227.5; DB 1; Length 260;
 Best Local Similarity 26.8%; Pred. No. 4e-13;
 Matches 69; Conservative 35; Mismatches 68; Indels 85; Gaps 7;
 QY 3 KALALIALALPAALALEGA-----SGFYQADAAHA-----KASSSLG 41
 DB 5 KFFSSILFSSLFSSNAQASEGSRSPYQADALAYAAERITHYPTPTGADKKISTV 64
 QY 42 S-----AKGSPRISAGYRINDLRFADVTRYRNYKQVPSTDEKL----- 81
 DB 65 SDFFNRIRAHSHIHPRVSGVDEGGMRIADYASYRKKWESNENSTKVEIKDKYKTKT 124
 QY 82 -----YSIGASATYDFDTQSPVKPYGLARLSLNR-----SYDFENS----- 118
 DB 125 EHQGNGSPFATSSLSGATYDPLKNDKRPYIGARVAYGHVAKHOVSEVTKTTVTSPRK 184
 QY 119 -----DSFSQTSGLGLVGLAVSVAYTPNVLDLADGARYNYIGKYNT 158
 DB 185 GGTGAGGPIKTPSKRPYHSHSISLGLVYAGVDFDIPKLLDGYRTHMGRLEN 244
 QY 159 VNVRSGLSAGVRYKF 175
 DB 245 TR-FKTHASLGMYRF 260
 RESULT 13
 OP28_NEIGO STANDARD; PRT; 234 AA.
 ID OP28_NEIGO P11297;
 AC P11297;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Opacity protein V28 precursor (Fragment).
 OS Neisseria gonorrhoeae.
 CC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 CC NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87002493; PubMed-3093085;
 RA Stern A., Brown M., Nickel P., Meyer T.F.;
 RT "Opacity genes in Neisseria gonorrhoeae: control of phase and
 antigenic variation."
 RL Cell 47:61-71(1986).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.

CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
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 CC -----
 DR EMBL; M14747; -; NOT_ANNOTATED_CDS.
 DR PIR; B24429; KONH8.
 DR InterPro: IPR003394; Opacity.
 DR Pfam; PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1
 FT SIGNAL 1
 FT CHAIN 2
 FT NON_TER 2
 FT CHAIN 2
 SQ SEQUENCE 234 AA; 26770 MW; 339ABD09C2FE75E4 CRC64;
 Query Match 25.7%; Score 224.5; DB 1; Length 234;
 Best Local Similarity 28.1%; Pred. No. 6.5e-13;
 Matches 64; Conservative 28; Mismatches 59; Indels 77; Gaps 7;
 QY 24 GPYQADAAHA-----KASSSLGSAR-----GFSRISAGYRINDLRF 61
 DB 8 GPYQADALAYVEHITHDHYPTPTGDKDKISTVDYRNRITSHHPRVSGVDEGGMRI 67
 QY 62 AVDTTRYKNY-----KQVSTDFKXSIGASATYDFDTQS 96
 DB 68 AADYARRKWKMDNRYSDIKELKNKONKRDJKTENGNGHFHAYVSLGLSAYVDFRLND 127
 QY 97 PVKPYGLARLSL--RASVDF-----NGSDFSQTS-----G 127
 DB 128 KFRPYIGARVAYGHVRSISDTKTKTFLTSSGGLNPVYTEENTONAHQNSIRRVG 187
 QY 128 LGVYAGSVAYTPNVLDLADGARYNYIGKYNTVNVRSGLSAGVRYKF 175
 DB 188 LGVYAGVGFDTPLKLLDADGARYHNMGRLENTR-FKTHASLGMYRF 234
 RESULT 14
 OP65_NEIGO STANDARD; PRT; 234 AA.
 ID OP65_NEIGO Q04885;
 AC Q04885;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA65 precursor (Fragment).
 OS Neisseria gonorrhoeae.
 CC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 CC NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-VPI;
 RX MEDLINE-93178439; PubMed-8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 epithelial cells."
 RL EMBO J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
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CC -----
 CC EMBL: Z18940: CAA79373.1; -
 DR PIR: S28617: S28617.
 DR InterPro: IPR003394: Opacity.
 DR Pfam: PF02462: Opacity; 1. Signal.
 KW Outer membrane; Multigene family; Signal.
 FT SIGNAL 1
 FT NON_TER <1 1
 FT CHAIN 2 >234 POTENTIAL.
 FT NON_TER 234 234 OPACITY PROTEIN OPA65.
 SQ SEQUENCE 234 AA; D66A0BA844AC2F1 CRC64;

Query Match 25.7%; Score 224.5; DB 1; Length 234;
 Best Local Similarity 28.9%; Pred. No. 6.5e-13;
 Matches 66; Conservative 25; Mismatches 60; Indels 77; Gaps 8;

OY 24 GFYVQADAAHA-----KASSSLGS-----AKGSPRISAGYRINDLRF 61
 DB 8 GPYVQADLAAYAEHITHDYPEPTGAKKQALSTVSDYFRNIRTHSIHRVSVGYDFGWMRI 67
 OY 62 ADVYRKYRKYQVST-----DFK-----LYSIGASAIYDFQTQSP 97
 DB 68 AADYARIRKMKWESNSIKKYVEDIKDKYKETEHOENGTFHVASISGLSTIYDFQISDK 127
 OY 98 VKPYLGARL-----SLNRASVDF-----NGSDSFQSTF-----G 127
 DB 128 IKPYIGVGVGVHVRHQVRSVGOETITVTPKNGTGGPVKSTSPIPAYHENSRRLG 187
 OY 128 LGLVAGVSAVTGPNVDLDAGYRNYIGKVTNKVNSGELSAGYRVKF 175
 DB 188 FGAAGAGVDVAPGLTLDAGYRHYHMGRLNTR-FKTHEASISGVYRIF 234

RESULT 15

OPAD_NEIGO STANDARD; PRT; 243 AA.

AC 004883;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA59 precursor (Fragment).
 GN OPAD.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-W., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT Variable opacity (Opa) outer membrane proteins account for the cell
 RT tropism displayed by Neisseria gonorrhoeae for human leukocytes and
 RT epithelial cells."

EMBO J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.

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 CC or send an email to license@lsb-slb.ch).

DR EMBL: Z18938: CAA79371.1; -
 DR PIR: S28629: S28629.
 DR InterPro: IPR003394: Opacity.
 DR Pfam: PF02462: Opacity; 1. Signal.
 KW Outer membrane; Multigene family; Signal.

FT NON_TER 1 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >243 OPACITY PROTEIN OPA59.
 FT NON_TER 243 243
 SQ SEQUENCE 243 AA; 27414 MW; 5930C73917436041 CRC64;

Query Match 25.5%; Score 223; DB 1; Length 243;
 Best Local Similarity 28.3%; Pred. No. 9.2e-13;
 Matches 67; Conservative 24; Mismatches 60; Indels 86; Gaps 7;

OY 24 GFYVQADAAHA-----KASSSLGSAK-----GSPRISAGYRINDLRF 61
 DB 8 GPYVQADLAAYAEHITHDYPEPTGKDKISTVSDYFRNIRTHSIHRVSVGYDFGWMRI 67
 OY 62 ADVYRKYRKYQVST-----DFK-----LYSIGASAIYDFQTQSP 97
 DB 68 AADYARIRKMKWESNSIKKYVEDIKDKYKETEHOENGTFHVASISGLSTIYDFQISDK 127
 OY 89 IYDFQTQSPVKPYLGARLSLNR-----ASYDFNG-----S 118
 DB 128 VYDFDGSREKPYIGMRVAVGVHVRHQVRSVGOETIAVTPYPONAASVYTNAPIRKLPH 187
 OY 119 DRSFQSTGLGVLAGVSAVTGPNVDLDAGYRNYIGKVTNKVNSGELSAGYRVKF 175
 DB 188 ESRSSISLFGAVAGVDITPNTLDAGYRHYHMGRLNTR-FKTHEASISGVYRIF 243

Search completed: October 28, 2002, 16:01:11
 Job time : 8.03013 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:56:04 ; Search time 20.0861 Seconds

(without alignments)
1507.218 Million cell updates/sec

Title: US-09-684-883-4

Sequence: 1 MKRAIALALPAAALAE.....VNTVKNVSGELSGAVRYKF 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	874	100.0	175	2	P95371
2	839.5	96.1	174	2	Q9RP18
3	838.5	95.9	174	16	P95372
4	836.5	95.7	174	2	Q9RP16
5	832.5	95.3	174	2	Q9R21
6	828.5	94.8	174	16	Q9RP17
7	824.5	93.3	174	2	P96943
8	813.5	93.1	174	2	P95343
9	246	28.1	186	16	Q9CM19
10	242.5	27.7	256	2	Q51126
11	242.5	27.7	256	2	Q51124
12	242	27.7	241	2	Q9AEB0
13	241.5	27.6	283	2	Q50943
14	239.5	27.4	262	2	Q07287
15	239.5	27.4	262	2	Q33388
16	238.5	27.3	234	2	Q9R719

17	238.5	27.3	234	2	007280
18	238.5	27.3	237	2	031176
19	238.5	27.3	259	2	051125
20	237.5	27.2	234	2	Q9R718
21	237.5	27.2	235	2	030753
22	237	27.1	257	2	050929
23	236.5	27.1	237	2	09K4T6
24	236.5	27.1	270	2	Q9RQV4
25	235.5	26.9	241	2	Q9K4T4
26	235	26.9	230	2	Q9R9A7
27	235	26.9	232	2	Q9K4T3
28	235	26.9	241	2	007274
29	234	26.8	232	2	Q9R3P5
30	234	26.8	241	2	007912
31	234	26.8	253	2	Q51303
32	232.5	26.6	242	2	Q9K4T8
33	232.5	26.6	272	2	051013
34	231	26.4	232	2	Q9K4T9
35	230.5	26.4	235	2	030752
36	230.5	26.4	240	2	007925
37	230.5	26.4	260	2	Q9R9A7
38	229.5	26.3	233	2	Q9K4T5
39	229	26.2	241	2	007273
40	228	26.1	238	2	031172
41	227	26.0	232	2	Q9R9A9
42	227	26.0	232	2	Q9R9A8
43	226	25.9	242	2	007279
44	225	25.7	234	2	030759
45	224.5	25.7	237	2	031175

ALIGNMENTS

RESULT 1					
P95371					
ID	P95371	PRELIMINARY;	PRT;	175 AA.	
AC	P95371				
DT	01-MAY-1997 (TREMBL)	03, Created)			
DT	01-MAY-1997 (TREMBL)	03, last sequence update)			
DT	01-DEC-2001 (TREMBL)	19, last annotation update)			
DE	OUTER MEMBRANE PROTEIN PRECURSOR.				
OS	Neisseria meningitidis.				
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.				
OX	NCBI:TaxID=487;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SRRAIN-MCH 88;				
RX	MEDLINE-9386904; PubMed-10456958;				
RA	Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;				
RT	"Bactericidal and cross-protective activities of a monoclonal antibody				
RT	directed against Neisseria meningitidis Nspa outer membrane protein."				
RL	Infect. Immun. 67:4955-4959(1999).				
DR	EMBL: U52067; AAB41578.1				
DR	InterPro: IPR003394; Opacity: 1.				
DR	Pfam: PF02462; Opacity: 1.				
KW	Signal.				
FT	SIGNAL.				
SQ	SEQUENCE	1	19	POTENTIAL.	
				DLEA8PFEFCGCCPEA CRC64;	
Query Match	175 AA;	18572 MW;			
Best Local Similarity	100.0%;	Score 874;	DB 2;	Length 175;	
Matches 175;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	MKRAIALALPAAALAGAGSFFVQAAAKAKSSISGSAKGFSPRTSGYRINDR	60		
DB	1	MKRAIALALPAAALAGAGSFFVQAAAKAKSSISGSAKGFSPRTSGYRINDR	60		
QY	61	FAYDYTRYKNYKQVPSTDFEFLYSIGASAIYDPTQSPVRYLGARLSLNRAVDENGSDS	120		
DB	61	FAYDYTRYKNYKQVPSTDFEFLYSIGASAIYDPTQSPVRYLGARLSLNRAVDENGSDS	120		
QY	121	FSQSTGLGVLAGVSTAVTPNVLDAGYRYNTYIGKYNVYKKNVSGELSGAVRYKF	175		


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Db 121 FSQSTGVLGVLGAGSYAVTPNVDDAGRYNYIGKVTNVKVRSGELSGAVRYKF 175
|||||
RESULT 2
ID Q9RP18 PRELIMINARY; PRT; 174 AA.
AC Q9RP18;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE SURFACE PROTEIN A.
GN NSPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8047;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
  among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
DR EMBL; AF175676; AAD53279.1; -.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity. 1.
SQ SEQUENCE 174 AA; 18357 MW; 0205A1DA1B7F005 CRC64;

Query Match 96.1%; Score 839.5; DB 2; Length 174;
Best Local Similarity 97.1%; Pred. No. 1.3e-62;
Matches 170; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 MKKALALIALALPAALAEAGSGFYVOADAAHAKASSLSGAKGSPRISAGYRINDLR 60
  |||||
DB 1 MKKALALIALALPAALAEAGSGFYVOADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNKYKQVPSDFKLYSIGASAIYDFDQSPVKKYLGARLSLNRAVDLGGSDS 120
  |||||
DB 61 FAVDYTRYKNKYK-APSTDFKLYSIGASAIYDFDQSPVKKYLGARLSLNRAVDLGGSDS 119
QY 121 FSQSTGVLGVLGAGSYAVTPNVDDAGRYNYIGKVTNVKVRSGELSGAVRYKF 175
  |||||
DB 120 FSQSTGVLGVLGAGSYAVTPNVDDAGRYNYIGKVTNVKVRSGELSGAVRYKF 174

RESULT 3
ID P95372 PRELIMINARY; PRT; 174 AA.
AC P95372;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN PRECURSOR.
GN NSPA OR NMA0862.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487, 65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=24063;
RA Martin D., Cadieux N., Hamel J., Rioux C., Brodeur B.R.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
RC MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jajelski K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;

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RT "Complete DNA sequence of a serogroup A strain of Neisseria
  meningitidis 22491.";
RL Nature 404:502-506(2000).
DR EMBL; U52068; AAB41580.1; -.
DR EMBL; AL162754; CAB84143.1; -.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity. 1.
KV Signal; Complete proteome.
FT SIGNAL 1
  19
SQ SEQUENCE 174 AA; 18355 MW; E8A4A1ADA4F6F009 CRC64;

Query Match 95.9%; Score 838.5; DB 16; Length 174;
Best Local Similarity 97.1%; Pred. No. 1.5e-62;
Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 MKKALALIALALPAALAEAGSGFYVOADAAHAKASSLSGAKGSPRISAGYRINDLR 60
  |||||
DB 1 MKKALALIALALPAALAEAGSGFYVOADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNKYKQVPSDFKLYSIGASAIYDFDQSPVKKYLGARLSLNRAVDLGGSDS 120
  |||||
DB 61 FAVDYTRYKNKYK-APSTDFKLYSIGASAIYDFDQSPVKKYLGARLSLNRAVDLGGSDS 119
QY 121 FSQSTGVLGVLGAGSYAVTPNVDDAGRYNYIGKVTNVKVRSGELSGAVRYKF 175
  |||||
DB 120 FSQSTGVLGVLGAGSYAVTPNVDDAGRYNYIGKVTNVKVRSGELSGAVRYKF 174

RESULT 4
ID Q9RP16 PRELIMINARY; PRT; 174 AA.
AC Q9RP16;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE SURFACE PROTEIN A.
GN NSPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
  among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
DR EMBL; AF175681; AAD53284.1; -.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity. 1.
SQ SEQUENCE 174 AA; 18355 MW; ECF6F38B9286800E CRC64;

Query Match 95.7%; Score 836.5; DB 2; Length 174;
Best Local Similarity 96.6%; Pred. No. 2.3e-62;
Matches 169; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 MKKALALIALALPAALAEAGSGFYVOADAAHAKASSLSGAKGSPRISAGYRINDLR 60
  |||||
DB 1 MKKALALIALALPAALAEAGSGFYVOADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNKYKQVPSDFKLYSIGASAIYDFDQSPVKKYLGARLSLNRAVDLGGSDS 120
  |||||
DB 61 FAVDYTRYKNKYK-APSTDFKLYSIGASAIYDFDQSPVKKYLGARLSLNRAVDLGGSDS 119
QY 121 FSQSTGVLGVLGAGSYAVTPNVDDAGRYNYIGKVTNVKVRSGELSGAVRYKF 175
  |||||
DB 120 FSQSTGVLGVLGAGSYAVTPNVDDAGRYNYIGKVTNVKVRSGELSGAVRYKF 174

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RESULT 5
ID Q9R2R1 PRELIMINARY; PRT; 174 AA.
AC Q9R2R1;

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RESULT 9	99CML19	PRELIMINARY	PRT;	186 AA.
ID	Q9CML19			
AC	Q9CML19;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	OPA.			
GN	OPA OR PM1025.			
OS	Pasteurella multocida.			
OC	Pasteurella; Proteobacteria; gamma subdivision; Pasteurellaceae;			
OC	Pasteurella.			
OX	NCBI_Taxid=747;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	STRATN=PM70;			
RX	MEDLINE=21145866; PubMed=11248100;			
RT	May B.Y., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;			
RL	"Complete genomic sequence of Pasteurella multocida pm70.";			
DR	Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).			
DR	EMBL: AE006143; AAK03109.1;			
DR	InterPro; IPR003394; Opacity.			
DR	Pfam; PF02462; Opacity; 1.			
FW	Complete proteome.			

QY	8	LIALALPAALALGASGYVOADAAH-----	KASSLGS-----	AKGFS 47
		: : : : : : : :	: : :	
Db	14	LESSAQAASSESGCPYYVADLAIYAERITHDYFKATGANNSTVSDFRNRRAISH 73		
QY	48	PRISAGYRINDLRFAVDTRYKNY-----	-----KQVSTDEKLY 82	
		: : : : : : : :	: : :	
Db	74	PRVSQVETGCDMRADADYASLRKNNNNKYSVNKLEKNHNKDKLTQNGENGTFFAAS 133		
QY	83	SIQASAIYFDQSPVAKPYLGLARLSLN--RASVD-----	-----FNQS 118	
		: : : : : : : :	: :	
Db	134	SLGLSAIYFQKINDKFKFKYLGARVAAYGHHVSHSIDSTKTTLEVSTHGAGADTKPTIYNGE 193		
QY	119	-----DSFQSTSGCLGVLAGVSYATLPWVDACGRYNYIGKYNATYKANRSGSLASGV 171		
		: : : : : : : :	: : :	
Db	194	STQNAVYHSHSIRRLGLGVAVAGVFDITPKLITDTGIRYHNMGRULENTR--PRTHEVSLGM 252		
QY	172	RVKF 175		

Db 253 RYHF 256

RESULT 11

Q51124 PRELIMINARY; PRT; 256 AA.

AC 051124: PRELIMINARY; PRT; 256 AA.
 AC 051124: PRELIMINARY; PRT; 256 AA.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE OPACITY OUTERMEMBRANE PROTEIN (FRAGMENT).
 GN OPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NCBI_TaxID=487;

RA Heckels J.E., Cannon J.G., Achtman M.,
 RA Hobbs M.M., Major J.B., Prasad P., Morelli G., Kusecek B.,
 RA "Recombinational reassortment among opa genes from ET-37 complex
 RT Neisseria meningitidis isolates of diverse geographical origins."
 RL Microbiology 144:157-166(1998).
 DR EMBL: U37255; AAC6101.1; -
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 FT NON_TER
 SQ SEQUENCE 256 AA; 28335 MW; 9DA1C6079C6DD13F CRC64;

Query Match 27.7%; Score 242.5; DB 2; Length 256;
 Best Local Similarity 27.9%; Pred. No. 1.3e-12;
 Matches 68; Conservative 34; Mismatches 65; Indels 77; Gaps 6;

QY 8 LILALPAALALGASGFVQADAAHA-----KASSLSGS-----AKGFS 47
 Db 14 LFSAAQAASEDSGHGPPYQADLAFAERITHDYPKAGANTSTVSDYFNIRAHSH 73
 QY 48 PRISAGYRINDLRFAYDYTRYKRYKQVPSTDFKL-----YS 83
 Db 74 PRYSVGYDEGGRKADYADYSTRKMKESNSYKVEDIADNFKETKEHQSGSFHAAS 133
 QY 84 IGASAIYDFDTOSPVKPYLGARLSLNR-----SVDFNGS----- 118
 Db 134 LGSALYDEKLDKDFKPYIGARVAGVHKQYHVSVEKTTTYSKPTATSPGGGLIQND 193
 QY 119 -----DSFSQSTGSLGVLAVSYAVTPNVDDLGRYRYNGKVTYKNSGELSAGV 171
 Db 194 PSKPPYHSHSISLGLGVIAGVEDITPKLTLDGTGRYHNMGRLENTF-FTHHEVSLGM 252
 QY 172 RVKF 175
 Db 253 RYRF 256

RESULT 12

Q9AE80 PRELIMINARY; PRT; 241 AA.

AC 09AE80: PRELIMINARY; PRT; 241 AA.
 AC 09AE80: PRELIMINARY; PRT; 241 AA.
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE OPACITY PROTEIN (FRAGMENT).
 GN OPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NCBI_TaxID=487;

RA "The opa locus of Neisseria gonorrhoeae MS11A is involved in
 RT epithelial cell invasion."
 RL Mol. Microbiol. 13:919-928(1994).
 DR EMBL: U13708; AAA74082.1; -
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 FT NON_TER
 SQ SEQUENCE 241 AA; 26923 MW; 4923ACF9484BF183 CRC64;

RA Popovic T., Schuurman I.G.A., Adegbola R.A., Zurth K., Gagneux S.,
 RA Platonov A.E., Riou J.Y., Caugant D.A., Nicolas P., Achtman M.,
 RT "Fit genotypes and escape variants of subgroup III Neisseria
 RT meningitidis during three pandemics of epidemic meningitis."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:5234-5239(2001).
 DR EMBL: AJ292238; CAC36361.1; -
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 FT NON_TER
 SQ SEQUENCE 241 AA; 26923 MW; 4923ACF9484BF183 CRC64;

Query Match 27.7%; Score 242; DB 2; Length 241;
 Best Local Similarity 30.1%; Pred. No. 1.4e-12;
 Matches 72; Conservative 30; Mismatches 57; Indels 80; Gaps 9;

QY 16 AALAEAG-SGFVQADAAHA-----KASSLSGS-----AKGFSRISAGY 54
 Db 4 AASEGSRSPYVQADLAFAERITHDYPKASGANTSTVSDYFNIRAHSHIPRVSVG 63
 QY 55 RINDLRFAYDYTRYKRYK-----KQVSTDFKLYSGAS 87
 Db 64 DGDWRIADYADYSTRKMKNDKSVTKRVQVKNKSGNRQDKTENQENGTFHAVSGLS 123
 QY 88 AIYDEDTOSPVKPYLGARLSLNR-RASVD-----FN-GS----- 118
 Db 124 AYIDPNTGSRFPYAGVAVAGVHSHSIDSTKTKTNTVLTPTNIPGPTIYNGSGTODA 183
 QY 119 -----DSFSQSTGSLGVLAVSYAVTPNVDDLGRYRYNGKVTYKNSGELSAGVRF 175
 Db 184 YHSHSIRLGLGVAGVGFDTPKLTLDGTGRYHNMGRLENTF-FTHHEVSLGVRYRF 241

RESULT 13

Q50943 PRELIMINARY; PRT; 283 AA.

AC 050943: PRELIMINARY; PRT; 283 AA.
 AC 050943: PRELIMINARY; PRT; 283 AA.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE OPA15063G.
 GN OPA15063G.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NCBI_TaxID=485;

Query Match 27.6%; Score 241.5; DB 2; Length 283;
 Best Local Similarity 28.7%; Pred. No. 1.9e-12;
 Matches 70; Conservative 26; Mismatches 69; Indels 79; Gaps 7;

QY 10 AALPAALALGASGFVQADAAHA-----SSLSGSAK-----FS 47
 Db 41 SLISAQAASEAMGPPYQADLAFAERITHDYPEPTGKGTISVSDYFNIRAHSHV 100
 QY 48 PRISAGYRINDLRFAYDYTRYKRYK-----KQVSTDFKLY 82
 Db 101 PRYSVGYDEGGRKADYADYSTRKMKNSVNIERYOEAHNSRIDKARNQENGTFHAVS 160
 QY 83 SIGASAIYDFDTOSPVKPYLGARLSLNR-RASVD-----PNG----- 117
 Db 161 SLGSAIYDFKLDKDFKPYIGARVAGVHSHSIDSTKTKTILTSYGVATPTTYDGP 220

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:55:03 ; Search time 24.7145 Seconds

(without alignments)
782,004 Million cell updates/sec

Title: US-09-684-883-6

Perfect score: 868

Sequence: 1 MKKALATLIALALPALAE.....VNTKVNRSGLSGAVRKF 174

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	868	100.0	174	17	AAW04893
2	854	98.4	174	17	AAW04891
3	838.5	96.6	175	17	AAW04892
4	834	96.1	174	17	AAW04894
5	771	88.8	155	22	AAI19895
6	735	15.6	170	16	AAW73911
7	133	15.3	25	17	AAW04912
8	99	11.4	353	22	AAW47447
9	96	11.1	212	22	AAW34556
10	92	10.6	257	22	AAW38252
11	92	10.6	568	17	AAW6210

12	91	10.5	359	16	AAW6294	Non-typable Haemop
13	89.5	10.3	339	21	AAW52873	Arabidopsis thalia
14	89.5	10.3	534	21	AAW09860	Arabidopsis thalia
15	89	10.3	369	21	AAW4589	Virulence gene pro
16	87.5	10.1	162	17	AAW6207	Attachment-invasio
17	87	10.0	16	17	AAW04901	N. meningitidis 60
18	87	10.0	350	9	AAW82053	Outer membrane pro
19	87	10.0	369	22	AAW59179	Protein associated
20	87	10.0	369	21	AAW96098	Actinobacillus ple
21	87	10.0	369	21	AAW97900	Actinobacillus ple
22	87	10.0	369	21	AAW65766	Cysteine protease
23	85.5	9.9	500	22	AAW65766	Porphorymonas ging
24	85.5	9.9	221	20	AAW34533	Chlamydia trachoma
25	85	9.8	797	20	AAW34400	Helicobacter pylori
26	84.5	9.7	708	19	AAW36955	H. pylori bacteria
27	84.5	9.7	708	21	AAW73022	The outer membrane
28	84	9.7	180	21	AAW78360	Arabidopsis thalia
29	84	9.7	180	21	AAW84612	Virulence gene pro
30	84	9.7	316	21	AAW52874	Actinobacillus ple
31	84	9.7	364	21	AAW44588	Actinobacillus ple
32	84	9.7	364	21	AAW96097	Arabidopsis thalia
33	84	9.7	364	21	AAW97899	Arabidopsis thalia
34	84	9.7	511	21	AAW09861	C glutamylom prote
35	83	9.6	261	22	AAW32501	Anaplasma marginal
36	81.5	9.4	282	19	AAW51090	Anaplasma marginal
37	81.5	9.4	282	21	AAW51090	Major antigenic pr
38	81.5	9.4	282	21	AAW04194	N. meningitidis 60
39	81	9.3	15	17	AAW04809	Actinobacillus ple
40	80.5	9.3	215	21	AAW96096	Actinobacillus ple
41	80.5	9.3	215	21	AAW97897	M. catarrhalis str
42	79.5	9.2	573	19	AAW68202	Arabidopsis thalia
43	79.5	9.2	581	21	AAW50574	Arabidopsis thalia
44	79.5	9.2	645	21	AAW50573	Arabidopsis thalia
45	79.5	9.2	704	20	AAW17210	H. pylori outer me

ALIGNMENTS

RESULT 1	AAW04893	standard; Protein; 174 AA.
ID	AAW04893	
AC	AAW04893	
XX		
DT	22-DEC-1996	(first entry)
XX		
DE	Proteinase K resistant N. meningitidis 22 kd surface protein.	
XX		
KW	Proteinase K resistant; Neisseria meningitidis;	
KW	Neisseria gonorrhoeae; antibody; detection; probe; surface protein.	
XX		
OS	Neisseria meningitidis strain 24063.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..19
FT	Protein	/label= sig_peptide
FT		20..174
FT		/label= mat_protein
XX		
PN	W05629412-A1.	
XX		
PD	26-SEP-1996.	
XX		
PF	15-MAR-1996;	96W0-CA00157.
XX		
PR	04-AUG-1995;	95US-0001983.
PR	17-MAR-1995;	95US-0406362.
XX		
PA	(IAFB-) IAF BIO VAC INC.	
XX		
PI	Brodeur BR, Hamel J, Martin D, Rioux C;	
XX		

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39041.
 XX Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 9; 117pp; English.
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 XX Sequence 174 AA:
 SQ
 Query Match 100.0%; Score 868; DB 17; Length 174;
 Best Local Similarity 100.0%; Pred. No. 5, 8e-85;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 OY 61 FAVDYTRYKNKAPSTDFKLYSIGASAIYDFPQSPVRYGARI.SLNRA.SVDLGGSDSF 120
 DB 61 FAVDYTRYKNKAPSTDFKLYSIGASAIYDFPQSPVRYGARI.SLNRA.SVDLGGSDSF 120
 OY 121 SQTSTGLGVLGVSVAVTNPVDDAGYRYNYIGKVTYKNNVRSGLSAGVRYKF 174
 DB 121 SQTSTGLGVLGVSVAVTNPVDDAGYRYNYIGKVTYKNNVRSGLSAGVRYKF 174

RESULT 2
 AAW04891
 ID AAW04891 standard; Protein; 174 AA.
 XX
 AC AAW04891;
 XX
 DT 22-DEC-1996 (first entry)
 XX
 DE Proteinase K resistant N. meningitidis 22 kD surface protein.
 XX
 KW Proteinase K resistant; Neisseria meningitidis;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
 XX
 OS Neisseria meningitidis strain 608B.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..174
 FT /label= mat_protein
 FT
 XX
 PN W09629412-A1.
 XX
 PD 26-SEP-1996.
 XX
 PF 15-MAR-1996; 96WO-CA00157.
 XX
 PR 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 XX
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39039.
 XX Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 1; 117pp; English.
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 XX Sequence 174 AA:
 SQ
 Query Match 98.4%; Score 854; DB 17; Length 174;
 Best Local Similarity 98.3%; Pred. No. 1, 8e-83;
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 OY 61 FAVDYTRYKNKAPSTDFKLYSIGASAIYDFPQSPVRYGARI.SLNRA.SVDLGGSDSF 120
 DB 61 FAVDYTRYKNKAPSTDFKLYSIGASAIYDFPQSPVRYGARI.SLNRA.SVDLGGSDSF 120
 OY 121 SQTSTGLGVLGVSVAVTNPVDDAGYRYNYIGKVTYKNNVRSGLSAGVRYKF 174
 DB 121 SQTSTGLGVLGVSVAVTNPVDDAGYRYNYIGKVTYKNNVRSGLSAGVRYKF 174

RESULT 3
 AAW04892
 ID AAW04892 standard; Protein; 175 AA.
 XX
 AC AAW04892;
 XX
 DT 22-DEC-1996 (first entry)
 XX
 DE Proteinase K resistant N. meningitidis 22 kD surface protein.
 XX
 KW Proteinase K resistant; Neisseria meningitidis;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
 XX
 OS Neisseria meningitidis strain MCH88.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..175
 FT /label= mat_protein
 FT
 XX
 PN W09629412-A1.
 XX
 PD 26-SEP-1996.
 XX
 PF 15-MAR-1996; 96WO-CA00157.
 XX
 PR 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 XX
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39040.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 8; 117pp; English.
 CC
 CC A protease K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 SQ Sequence 175 AA;
 Query Match 96.6%; Score 838.5; DB 17; Length 175;
 Best Local Similarity 97.1%; Pred. No. 8.5e-82;
 Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNNK-APSDPFLKYSIGASAIYDPTQSPVKRYLGARLSLNKASVDLGSDS 119
 DB 61 FAVDYTRYKNNKQVPSDFKLYSIGASAIYDPTQSPVKRYLGARLSLNKASVDLGSDS 120
 QY 120 FSGTSTGLVAGSYAVTPNVDLDAGYRYNYIGKNTYKNNVNSGELSAGYRYKF 174
 DB 121 FSGTSTGLVAGSYAVTPNVDLDAGYRYNYIGKNTYKNNVNSGELSAGYRYKF 175
 RESULT 4
 AAM04894
 ID AAM04894 standard; Protein; 174 AA.
 AC AAM04894;
 XX
 DT 22-DEC-1996 (first entry)
 XX
 DE Protease K resistant N. meningitidis 22 kD surface protein.
 XX
 KW Protease K resistant; Neisseria meningitidis;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein;
 XX
 OS Neisseria meningitidis strain b2.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..174
 FT /label= mat_protein
 PN W09629412-A1.
 XX
 PD 26-SEP-1996.
 XX
 PF 15-MAR-1996; 96WO-CA00157.
 XX
 PR 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 XX
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39042.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 10; 117pp; English.
 CC
 CC A protease K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 SQ Sequence 174 AA;
 Query Match 96.1%; Score 834; DB 17; Length 174;
 Best Local Similarity 95.4%; Pred. No. 2.6e-81;
 Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNNK-APSDPFLKYSIGASAIYDPTQSPVKRYLGARLSLNKASVDLGSDS 120
 DB 61 FAVDYTRYKNNKQVPSDFKLYSIGASAIYDPTQSPVKRYLGARLSLNKASVDLGSDS 120
 QY 121 SGTSTGLVAGSYAVTPNVDLDAGYRYNYIGKNTYKNNVNSGELSAGYRYKF 174
 DB 121 SGTSTGLVAGSYAVTPNVDLDAGYRYNYIGKNTYKNNVNSGELSAGYRYKF 174
 RESULT 5
 AAB19895
 ID AAB19895 standard; Protein; 155 AA.
 AC AAB19895;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE Neisseria meningitidis Nspa protein.
 XX
 KW Nspa; infection; diagnosis; therapy; vaccine; meningococcal B.
 KW Neisseria meningitidis.
 XX
 OS Neisseria meningitidis.
 XX
 FH Key Location/Qualifiers
 FT Region 6..17
 FT /note= "transmembrane beta-strand"
 FT Region 18..26
 FT /note= "surface-exposed connecting loop"
 FT Region 27..37
 FT /note= "transmembrane beta-strand"
 FT Region 40..50
 FT /note= "transmembrane beta-strand"
 FT Region 51..62
 FT /note= "surface-exposed connecting loop"
 FT Region 63..74
 FT /note= "transmembrane beta-strand"
 FT Region 78..88
 FT /note= "transmembrane beta-strand"
 FT Region 89..104
 FT /note= "surface-exposed connecting loop"
 FT Region 105..114
 FT /note= "transmembrane beta-strand"
 FT Region 118..130

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FT      /note="Transmembrane beta-strand"
FT      131..145
FT      /note="Surface-exposed connecting loop"
FT      146..155
FT      Region
FT      /note="transmembrane beta-strand"
PN      WO200071725-A2.
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XX      30-NOV-2000.
XX
XX      19-MAY-2000; 2000WO-IB00828.
XX
XX      19-MAY-1999; 99GB-0011692.
XX      19-AUG-1999; 99GB-0019705.
XX      09-MAR-2000; 2000GB-0005730.
XX
XX      (CHIR-) CHIRON SPA.
XX
XX      Giuliani MM, Pizzi M, Rappuoli R;
XX      WPI; 2001-025167/03.
XX
XX      Novel composition comprising first and second biological molecules from
XX      a Neisseria bacterium, useful as vaccines or immunogenic compositions
XX      for treating Neisseria infections
XX
XX      Example 12; Fig 32; 126pp; English.
XX
XX      The present sequence is that of the Neisseria meningitidis Nspa
XX      protein, which contains 8 transmembrane beta strands and 4
XX      surface-exposed connected loops. Recombinant Nspa is being
XX      developed as a vaccine for the prevention of meningococcal
XX      disease caused by all serotypes. The invention provides
XX      combination compositions comprising: (i) 2 or more Neisseria
XX      proteins; (ii) 2 or more different Neisseria nucleic acids; or
XX      (iii) mixtures of 1 or more Neisseria protein and 1 or more
XX      Neisseria nucleic acid. The proteins and nucleic acids are
XX      preferably from different Neisseria spp., especially Neisseria
XX      meningitidis and Neisseria gonorrhoeae, but may be from the same
XX      species. A claimed composition includes the Nspa protein,
XX      CC preferably in mature form. The compositions are used e.g. as
XX      immunogenic compositions, vaccines or diagnostic reagents. They
XX      are used to treat or prevent Neisseria infection, to detect the
XX      presence of Neisseria bacteria or of antibodies raised against
XX      Neisseria bacteria, and/or as reagents which can raise antibodies
XX      against Neisseria bacteria.
XX
XX      Sequence 155 AA:
XX
XX      Query Match      88.8%; Score 771; DB 22; Length 155;
XX      Best Local Similarity 98.1%; Pred. No. 1.2e-74;
XX      Matches 152; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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XX      20 EGASGFVQADAAHAKASSLSGAKGSPRISAGYRINDLRFADVTRYKNKAPSTDK 79
XX      |||||
XX      Db      1 EGASGFVQADAAHAKASSLSGAKGSPRISAGYRINDLRFADVTRYKNKAPSTDK 60
XX
XX      QY      80 LYSIGASAIYDFDTQSPVKRYLGARLSLNKASAYDLGSDSFSQTSGLGLVAGSYAVVP 139
XX      |||||
XX      Db      61 LYSIGASAIYDFDTQSPVKRYLGARLSLNKASAYDLGSDSFSQTSGLGLVAGSYAVVP 120
XX
XX      QY      140 NVLDAGRYNTYIGKVTYKANKVNSGELSAGYRVKF 174
XX      |||||
XX      Db      121 NVLDAGRYNTYIGKVTYKANKVNSGELSAGYRVKF 155
XX
XX      RESULT 6
XX      AAR73911
XX      ID      AAR73911 standard; protein; 170 AA.
XX      AC      AAR73911;
XX      XX
XX      DT      05-DEC-1995 (first entry)

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XX      Neisseria meningitidis opacity related protein POPM3.
DE      Neisseria meningitidis; opacity related protein POPM3; vaccine;
XX      Neisseria meningitidis related homologous antigenic sequence; MRHA5; RV-1;
XX      immunosassay; diagnosis; treatment; prophylactic; bacterial;
XX      viral.
XX
XX      Neisseria meningitidis.
XX
XX      WO9509232-A.
XX
XX      06-APR-1995.
XX
XX      28-SEP-1994; 94WO-CA00516.
XX
XX      28-SEP-1993; 93US-0127499.
XX
XX      (SHAR/) SHARMA L R.
XX      (VALS/) VAN ALSTYNE D.
XX
XX      Sharma LR, Van Alstyne D;
XX      WPI; 1995-147431/19.
XX
XX      New peptide(s) and corresp. antibodies for the treatment of
XX      meningitis - the peptide(s) corresp. to homologous antigenic
XX      sites on bacterial and viral agents and on chemokine(s), used for
XX      detecting and preventing meningitis
XX
XX      Claim 47; Fig 5/10; 98pp; English.
XX
XX      AAR73911 is the Neisseria meningitidis opacity related protein POPM3.
XX      It contains the meningitis related antigenic sequences (MRHA5)
XX      claimed in AAR73889 and AAR73901, which are recognised by a monoclonal
XX      antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHA5
XX      peptides may be used in immunoassays to diagnose the presence of
XX      bacterial and/or viral meningitis agents in a sample, or in
XX      prophylactic and therapeutic meningitis treatments. The peptides may
XX      also be used as vaccines against meningitis.
XX      NB: Identified by matching corresponding MRHA5 peptides.
XX
XX      Sequence 170 AA:
XX
XX      Query Match      15.6%; Score 135; DB 16; Length 170;
XX      Best Local Similarity 26.3%; Pred. No. 1.8e-06;
XX      Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;
XX
XX      6 ATLINALPAAALAEASGFVQADAAH-----AKASSLSG-----AKG 45
XX      ::::: ||: | :|: ||||| :|: |
XX      Db      15 SSLFSSAAQAASDESRSPYVQADLAYAERITHDYPOATGANNSTVSDFENIRAHS 74
XX
XX      QY      46 FSPRISAGYRINDLRFADVTRYKNY-----KAPSTDFK 79
XX      ||: | | | | | :|: |
XX      Db      75 IHPKSVGTIDGGMFLADYASIRKMNKNSVYTKELKHNKKDLKTENDENGTFHA 134
XX
XX      QY      80 LYSIGASAIYDFDTQSPVKRYLGARLSLN--RASVD 113
XX      ||: ||||| :|: ||||| :|: |
XX      Db      135 ASSIGLSAIYDFKLGKRFKPYIGARVAAGVHRHSID 170
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XX      RESULT 7
XX      AAM04912
XX      ID      AAM04912 standard; protein; 25 AA.
XX      AC      AAM04912;
XX      XX
XX      DT      22-DEC-1996 (first entry)
XX
XX      N. meningitidis 608B peptide CS-857.
XX
XX      Proteinase K resistant; Neisseria meningitidis; epitope; mapping;
XX      Neisseria gonorrhoeae; antibody; detection; probe; surface protein.

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XX OS Synthetic.
XX PF WO629412-A1.
XX PN 26-SEP-1996.
XX PD
XX PF 15-MAR-1996; 96WO-CA00157.
XX PR 04-AUG-1995; 95US-0001983.
XX PR 17-MAR-1995; 95US-0406362.
XX PA (IAFB-) IAF BIO VAC INC.
XX PI Brodeur BR, Hamel J, Martin D, Rioux C;
XX WPI: 1996-443187/44.
XX DR
XX PT Neisseria meningitidis antigen, highly conserved between different
XX PT strains - useful for prodn. of antibodies for immunisation against,
XX PT or diagnosis of, N. meningitidis infection
XX PS Claim 24; Page 84; 117pp; English.
XX CC Example 9 describes the epitope mapping of the 22 kD
XX CC N. meningitidis protein. Identification was accomplished
XX CC using 18 overlapping synthetic peptides (AAW04895 to AAW04912).
XX SQ Sequence 25 AA;

Query Match 15.3%; Score 133; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FAVDYTRYKNYKAPSTDFFKYSIGA 85
DB 1 FAVDYTRYKNYKAPSTDFFKYSIGA 25

RESULT 8
AAB47447
ID AAB47447 standard; Protein; 353 AA.
XX AC AAB47447;
XX DT 31-OCT-2001 (first entry)
XX DE MOMP P5.
XX KW surface exposed loop; major outer membrane protein P5; MOMP P5;
XX KW non-typeable H. influenzae; nHi; LBI(f) peptide; B cell epitope;
XX KW otitis media; sinusitis; conjunctivitis;
XX KW lower respiratory tract infection.
XX OS Haemophilus influenzae.
XX FH Key
XX FT 38..57 Location/Qualifiers
XX FT /label= Loop 1
XX FT /note= "Extracellular domain"
XX FT 89..100
XX FT /label= Loop 2
XX FT /note= "Extracellular domain"
XX FT 136..150
XX FT /label= Loop 3
XX FT /note= "Extracellular domain"
XX FT 181..204
XX FT /label= Loop 4
XX FT /note= "Extracellular domain"
XX PN WO200161013-A1.
XX PD 23-AUG-2001.

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XX XX 13-FEB-2001; 2001WO-EP01556.
XX XX 15-FEB-2000; 2000GB-0003502.
XX XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PA Berthet FJ, Denoel P, Poolman J, Thonnard J;
XX PI WPI: 2001-522599/57.
XX DR
XX PT Recombinant bacterial outer membrane protein where one or more
XX PT surface-exposed loops are modified is useful as a vaccine to prevent or
XX PT treat Haemophilus influenzae infection or associated disease, e.g.,
XX PT otitis media and conjunctivitis -
XX PS Disclosure; Fig 1; 29pp; English.
XX CC This sequence represents the major outer membrane protein P5 of
XX CC non-typeable H. influenzae. One or more surface exposed loops of this
XX CC protein may be replaced with a modified peptide of the invention. Each
XX CC of these peptides contain an LBI(f) peptide which is a 19 amino acid
XX CC peptide derived from the sequence of MOMP P5 from strain nH1128,
XX CC representing amino acids Arg117 to Gly135. This peptide represents the
XX CC third exposed loop of P5 and is a potential B cell epitope. The loops
XX CC of the invention are modified in terms of being in a non-native
XX CC environment in the recombinant outer membrane protein. The modified
XX CC MOMP P5 may be used to induce an immune response in a mammal to
XX CC prevent or treat Haemophilus influenzae infection or associated
XX CC disease, e.g., otitis media, sinusitis, conjunctivitis, or lower
XX CC respiratory tract infection.
XX SQ Sequence 353 AA;

Query Match 11.4%; Score 99; DB 22; Length 353;
Best Local Similarity 24.8%; Pred. No. 0.035;
Matches 53; Conservative 29; Mismatches 92; Indels 40; Gaps 9;

QY 1 MKKALATLIALALPAAALAEAG--SGEYVOADAHHKASSSGS-----AKGPS 47
DB 1 MKKTAIALVVAAGLAASVAAPOENTFYAGVAAQASFDGLRALAREKVGYHRNSFT 60
QY 48 PRISAGYRI--NDLRPAV-----DYTRYKNYKAPSTDFFKYSIGA--SAIYDFYQSPV 97
DB 61 YGVFGGYOILNONNLGLAVELGYDDFGRAKGRKGVKHTVHNGHLSLKGSYEVLG 120
QY 98 KPYLGARLSLRASVVDGSDSFSQSTG-----LGVLA-GVSYAVYPNDLDAGY-- 147
DB 121 DYGKAGVALVRSDYKLYNENSTLKKLGHHRRASGLPFAVGAEYAVLPFLAVRLEYOM 180
QY 148 ----RYNYIGKVTYVNRVS--GELSAGYRVKE 174
DB 181 LTRYGKTRYPQDKPMTALNPNWIGSINAGISYRF 214

RESULT 9
AAU34556
ID AAU34556 standard; Protein; 212 AA.
XX AC AAU34556;
XX DT 14-FEB-2002 (first entry)
XX DE E. coli cellular proliferation protein #137.
XX KW Antisense; prokaryotic cellular proliferation protein;
XX KW antibiotic; antibacterial; drug design.
XX OS Escherichia coli.
XX PN WO200170955-A2.
XX PD 27-SEP-2001.

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XX 21-MAR-2001; 2001WO-US09180.
 PF 21-MAR-2000; 2000US-191078P.
 XX 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX (ELIT-) ELITRA PHARM INC.
 PA Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX WPI; 2001-611495/70.
 DR N-PSDB; AAS52415.
 XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 PS Example 3; Seq ID No 10149; 511pp; English.
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 CC Sequence 212 AA:
 SQ
 Query Match 11.1%; Score 96; DB 22; Length 212;
 Best Local Similarity 23.7%; Pred. No. 0.037;
 Matches 53; Conservative 28; Mismatches 77; Indels 66; Gaps 11;
 QY 1 MKKALATLIALA--LPAALAEAGSGFYQADAAHAK---ASSLSGSAKFSPRISAGY 54
 DB 1 MKKLTVALAVTTLLSGSAFAHEAGFEFMRGSAIVRPTGAGGTGLSGFSY----- 54
 QY 55 RINDLRFAVDYTRYKNYKA-----PSTDFKLYSIGASAIYDF----- 91
 DB 55 -TNNTOGLGTF---YMAIDNIGVELLAATPFR-HKVTGATGDIATVHLLPPTLMAQW 108
 QY 92 ---DTQSPKPYLYGARLS-----LNRAVDLGSDSFSQSTGTGLAGVSYAVTPN 140
 DB 109 YFGDSSSKVRPYVGAVNTTFFDNDGKKTGSLDLSKMGCAAGGVGYDYLINRD 168
 QY 141 -----VDLDAGYRYNYIGKVNTRYKVRSGE---LSAGVR 171
 DB 169 WLVNMSVYMDIDITTYANK-LGCAQCHDSVLDLPWFVFMFSGAYR 211
 RESULT 10
 AAU38252
 ID AAU38252 standard; Protein; 257 AA.
 XX AC AAU38252;
 XX

DT 14-FEB-2002 (first entry)
 XX
 DE *Salmonella typhi* cellular proliferation protein #143.
 XX
 KW Antisense: prokaryotic cellular proliferation protein;
 KM antibiotic; antibacterial; drug design.
 XX
 OS *Salmonella typhi*.
 XX
 PN WO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX WPI; 2001-611495/70.
 DR N-PSDB; AAS56111.
 XX
 DR New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 PS Example 3; Seq ID No 13845; 511pp; English.
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 CC Sequence 257 AA:
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 Query Match 10.6%; Score 92; DB 22; Length 257;
 Best Local Similarity 23.7%; Pred. No. 0.13;
 Matches 53; Conservative 28; Mismatches 77; Indels 66; Gaps 12;
 QY 1 MKKALATLIALA--LPAALAEAGSGFYQADAAHAK---ASSLSGSAKFSPRISAGY 54
 DB 27 MKKFTVALAVTTLLSGSAFAHEAGFEFMRGSAIVRPTGAGGTGLHNGFD--VS-- 81
 QY 55 RINDLRFAVDYTRYKNYKA-----PSTDFKLYSIGASAIYDF----- 91
 DB 82 ---NNTQGLGTF---YMAIDNIGVELLAATPFR-HKVTGATGDIATVHLLPPTLMAQW 134
 QY 92 ---DTQSPKPYLYGARLS-----LNRAVDLGSDSFSQSTGTGLAGVSYAVTPN 140
 DB 135 YFGDSSSKVRPYVGAVNTTFFDNDGKKTGSLDLSKMGCAAGGVGYDYLINRD 194

biologically active material, and

CC microbial host , pref. E.coli, Sporodoptera frugiperda or a mucosal

CC pathogen. Fimbria protein (FP) produced by this process is claimed.
CC The FP protein migrates in polyacrylamide gels to a posn. equiv. to
CC a mol. wt. of 25.5 kD or 37.5 kD.

SO Sequence 359 AA;

Query Match 10.5%; Score 91; DB 16; Length 359;

Best Local Similarity 23.68; Pred. No. 0.26; Mismatches 82; Indels 64; Gaps 12;

Matches 54; Conservative 29; Mismatches 82; Indels 64; Gaps 12;

DB 1 MKKATLALPAALAECA--SGFYVADAA--HAKASSISGAKSPRISAG 53

DB 1 MKKATLALPAALAECA--SGFYVADAA--HAKASSISGAKSPRISAG 53

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DB 1 MKKATLALPAALAECA--SGFYVADAA--HAKASSISGAKSPRISAG 53

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DB 1 MKKATLALPAALAECA--SGFYVADAA--HAKASSISGAKSPRISAG 53

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 14-MAY-1999; 99US-0134768.

PR 14-MAY-1999; 99US-0134941.

PR 14-MAY-1999; 99US-0135124.

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PR 26-JUL-1999; 99US-0145276.
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PR 02-AUG-1999; 99US-0146386.
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PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
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PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
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PR 13-AUG-1999; 99US-0148565.
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PR 17-AUG-1999; 99US-0149175.
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PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153738.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155658.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
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PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.

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PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 10.3%; Score 89.5; DB 21; Length 339;
Best Local Similarity 27.7%; Pred. No. 0.35;
Matches 39; Conservative 20; Mismatches 53; Indels 29; Gaps 8;

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QY 39 SLSGAKG-----SPRISAGYRINDIRFAVDY--TRKNYKAPSTDFKLYSIGASAIY 89
DB 18 SSSAKMFIESFKVESPVK--YTENETHSVYDETTEVHAKTVNGYQWIVKPKIVKY 75
QY 90 DFDQSPVKPYLGARLSLRASVDLGSDFRSTGTGLGVIA--GYSYAVTPNWDIDAG 146
DB 76 DFKTDIRV-PKLGVL-----VGLGNGGSTLTA---GVIANREGISMATKDKVQ---- 121
QY 147 YRYNYIGKRVNTKKNVRSGLS 167
DB 122 -QANFGSLTQASSIRVGSFN 141

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RESULT 14
AAG09860
ID AAG09860 standard; Protein; 534 AA.

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AC AAG09860;
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DT 17-OCT-2000 (first entry)

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DE Arabidopsis thaliana protein fragment SEQ ID NO: 7956.

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XX Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

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OS Arabidopsis thaliana.

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XX EP1033405-A2.

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XX PD 06-SEP-2000.

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XX PF 25-FEB-2000; 2000EP-0301439.

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XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
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PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
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PR 30-APR-1999; 99US-0132407.
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PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.

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PR 14-MAY-1999; 99US-0134218.
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PR 27-MAY-1999; 99US-0136782.
PR 28-MAY-1999; 99US-0137222.
PR 01-JUN-1999; 99US-0137528.
PR 03-JUN-1999; 99US-0137502.
PR 04-JUN-1999; 99US-0137724.
PR 07-JUN-1999; 99US-0138094.
PR 08-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
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PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
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PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 18-JUN-1999; 99US-0139817.
PR 21-JUN-1999; 99US-0139899.
PR 22-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 23-JUN-1999; 99US-0140695.
PR 24-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 29-JUN-1999; 99US-0141287.
PR 30-JUN-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
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PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 16-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 23-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.

PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151308.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156596.
PR 29-SEP-1999; 99US-0157117.
PR 04-OCT-1999; 99US-0157753.
PR 05-OCT-1999; 99US-0157865.
PR 06-OCT-1999; 99US-0158029.
PR 07-OCT-1999; 99US-0158232.
PR 08-OCT-1999; 99US-0158369.
PR 12-OCT-1999; 99US-0159283.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160778.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 21-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.

PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 10.3%; Score 89.5; DB 21; Length 534;
 Best Local Similarity 27.7%; Pred. No. 0.63;

Matches 39; Conservative 20; Mismatches 53; Indels 29; Gaps 8;

QY 39 SLGAKGF-----SPRISAGYRINDLRPAVDY--TRYKNYKAPSTDFLYSIGASAIY 89
 DB 18 SFSAKMFIKESFKVESPNVK--YTENEIHSYDEETTEVYHEKTVNGTYQMYKPKTVKY 75
 QY 90 DEDTQSPVKPYLGARLSLNRAVDLGSDSFSTGSLGVL--GVSVAVTPNVDLDAG 146
 DB 76 DFKTDIVY-PLGVML-----VGLGGNGSTLTLA--GVIANKEGISMATKDKVQ---- 121
 QY 147 YRYNYIGKVTYKVRSGELS 167
 DB 122 -QANYFGLQASSIRYGSFN 141

RESULT 15
 AAB44589

ID AAB44589 standard; Protein; 369 AA.

XX AAB44589;

DT 08-FEB-2001 (first entry)

DE Virulence gene protein #69.

XX Virulence gene; antibacterial; vaccine; bacterial infection;

KW septicemia; bronchopneumonia; rhinitis; wound infection.

XX Actinobacillus pleuropneumoniae.

PN WO200061724-A2.

PD 19-OCT-2000.

PF 06-APR-2000; 2000WO-US09218.

PR 09-APR-1999; 99US-0128689.

PR 10-SEP-1999; 99US-0153453.

XX (PHAA) PHARMACIA & UPJOHN INC.

PI Lowery DE, Fuller TE, Kennedy MJ;

DR WPI; 2000-647422/62.

DR N-PSDB; AAC79664.

PT Attenuated Pasteurellaceae bacteria comprising mutations in virulence
 genes, useful as a live attenuated vaccine against bacterial infections

XX Claim 39; Pages 308-309; 322pp; English.

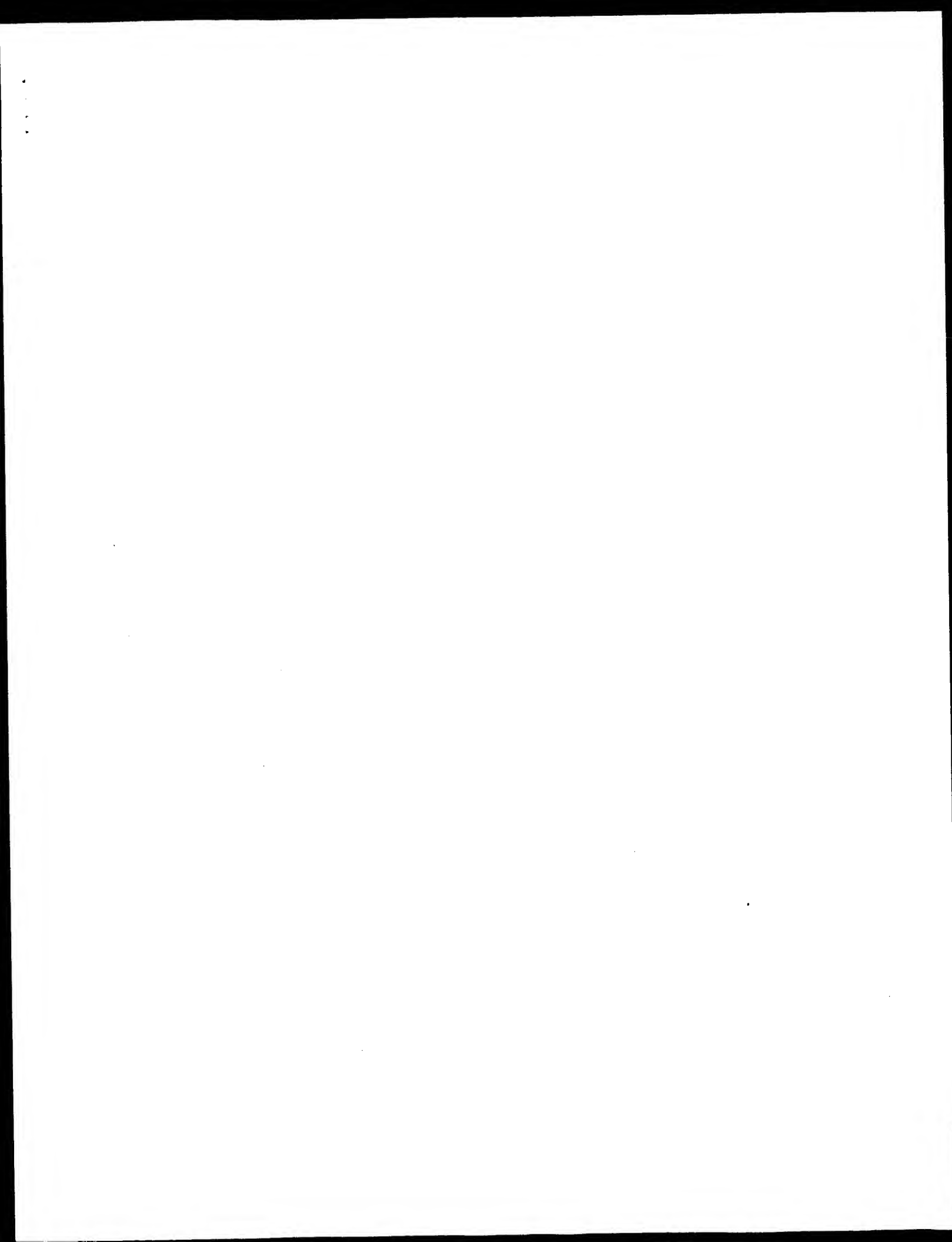
XX The family Pasteurellaceae encompasses several pathogens that infect a
 CC wide variety of animals. The present invention relates to virulence genes
 CC from Pasteurellaceae. The present sequence is a protein encoded by one
 CC such virulence gene. The virulence gene of the present invention may be
 CC mutated in order to produce an inactive gene. The inactive virulence gene
 CC may in turn be used to produce a vaccine, which is useful for treating
 CC bacterial infections such as septicemias, bronchopneumonias, rhinitis and

CC wound infections.
 XX Sequence 369 AA;

Query Match 10.3%; Score 89; DB 21; Length 369;
 Best Local Similarity 21.5%; Pred. No. 0.44;
 Matches 49; Conservative 36; Mismatches 85; Indels 58; Gaps 11;

QY 1 MKKALTLTALALPAALAEGA--SGFYVQADAAHAKASSISGSAK--GFSPR----- 49
 DB 1 MKKSLVALAVLS--AAAVQAAPQONTFFYAGAKVGQSPFHGCVNQLKSGHDDRYNDKTRK 58
 QY 50 -----TSAGYRI--NDLRPAVD--TRYKNYKAPSTDFLYSIGASAIY----- 89
 DB 59 YGINRNSVTYGVPGGTYQLNQNNGFLAELGYDYGVRKGVNDEFRYVKSASHGINTALK 118
 QY 90 -DEDTQSPVKPYLGARLSLNRAVDLGSDSFSTGSLGVL--GVSVAVTPNVDLDAG 141
 DB 119 PSYEVLPDLDVYGVKGIYAVVRNDYKKYGAENTNESTFKFKLKAATIIAGAVEYALP-- 176
 QY 142 DIDAGYRYNYIGKVTYKVR--VRSG-----ELSAQVRVKE 174
 DB 177 ELAARVEYQYLNKAGNLKALVRSSTQDVDFQYAPDISHVWAGISYRF 224

Search completed: October 28, 2002, 16:00:39
 Job time : 25.7145 secs



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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:58:54 ; Search time 9.48637 Seconds

(without alignments)
448.017 Million cell updates/sec

Title: US-09-684-883-6

Sequence: 1 MKKALATLIALPAALAE.....VNTKVNKSGELSGRVK 174

Scoring table: BLOSUM62

GAPOP 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Issued_Patents_AA.*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/PTCUTS.COMB.pep.*
7: /cgn2_6/ptodata/1/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	868	100.0	174	4	US-08-913-362-6
2	854	98.4	174	4	US-08-913-362-2
3	847.5	97.6	175	4	US-08-913-362-30
4	838.5	96.6	175	4	US-08-913-362-4
5	834	96.1	174	4	US-08-913-362-8
6	135	15.6	170	1	US-08-127-499A-20
7	133	15.3	25	4	US-08-482-847-20
8	133	15.3	25	4	US-08-482-847-20
9	93	10.7	359	1	US-08-457-997B-2
10	93	10.7	359	3	US-08-457-997B-2
11	92	10.6	568	5	US-08-467-722A-2
12	87	10.0	16	4	US-08-913-362-15
13	81.5	9.4	282	4	US-08-913-362-6
14	81.5	9.4	282	4	US-08-913-362-6
15	81	9.3	15	4	US-08-913-362-23
16	79.5	9.2	573	4	US-09-336-447A-15
17	79	9.1	15	4	US-08-913-362-18
18	79	9.1	207	2	US-08-381-881-6
19	79	9.1	207	4	US-09-281-221-6
20	79	9.1	610	4	US-09-336-447A-11
21	79	9.1	624	4	US-09-336-447A-7
22	79	9.1	889	4	US-09-336-447A-15
23	78	9.0	15	4	US-08-913-362-14
24	78	9.0	15	4	US-08-913-362-16
25	78	9.0	2123	4	US-08-968-685A-10
26	77.5	8.9	409	4	US-09-066-046-31
27	77.5	8.9	409	4	US-09-066-047-19

28	77	8.9	15	4	US-08-913-362-11	Sequence 11, Appl
29	77	8.9	15	4	US-08-913-362-13	Sequence 13, Appl
30	77	8.9	433	2	US-08-883-515-2	Sequence 2, Appl
31	76	8.8	15	4	US-08-913-362-17	Sequence 17, Appl
32	76	8.8	15	4	US-08-913-362-24	Sequence 24, Appl
33	75.5	8.7	286	1	US-08-382-184-3	Sequence 3, Appl
34	75.5	8.7	286	2	US-08-641-356-3	Sequence 3, Appl
35	75.5	8.7	286	4	US-09-132-528-4	Sequence 4, Appl
36	75.5	8.7	286	4	US-08-875-494-3	Sequence 4, Appl
37	75.5	8.7	286	4	US-08-382-184-2	Sequence 2, Appl
38	75.5	8.7	325	1	US-08-382-184-2	Sequence 2, Appl
39	75.5	8.7	325	2	US-08-641-356-2	Sequence 2, Appl
40	75.5	8.7	325	4	US-09-132-528-2	Sequence 2, Appl
41	75.5	8.7	325	4	US-08-875-494-2	Sequence 3, Appl
42	75.5	8.7	325	4	US-08-875-494-2	Sequence 2, Appl
43	75.5	8.7	325	4	US-09-559-366-2	Sequence 2, Appl
44	75.5	8.7	325	4	US-09-559-366-3	Sequence 3, Appl
45	75.5	8.7	332	4	US-08-818-112-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-08-913-362-6

; Sequence 6, Application US/08913362
; Patent No. 6287574

; GENERAL INFORMATION:

; APPLICANT: Brodeur, Bernard R

; APPLICANT: Martin, Denis

; APPLICANT: Hamel, Josee

; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN

; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/913,362

; FILING DATE: 13-NOV-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/406,362

; FILING DATE: 17-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/001,983

; FILING DATE: 04-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Bent, Stephen A.

; REGISTRATION NUMBER: 29,768

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 174 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: Protein

Query Match 100.0%; Score 868; DB 4; Length 174;

Best Local Similarity 100.0%; Pred. No. 5.6e-92;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALALAGAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALALAGAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRKKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSINRASVDLGSDSF 120
Db 61 FAVDYTRKKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSINRASVDLGSDSF 120

QY 121 SQTSTGLVLAGVSYAVTPNVDDAGYRNYIGKVTYKKNVRSGLSAGYRVKF 174
Db 121 SQTSTGLVLAGVSYAVTPNVDDAGYRNYIGKVTYKKNVRSGLSAGYRVKF 174

RESULT 2

US-08-913-362-2
Sequence 2, Application US/08913362

Patent No. 6287574
GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis

APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500
CITY: Washington

STATE: D.C.
COUNTRY: USA

ZIP: 20007-5109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids

TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-913-362-2

Query Match 98.4%; Score 854; DB 4; Length 174;
Best Local Similarity 98.3%; Pred. No. 2.3e-90;

Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALALAGAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALALAGAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRKKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSINRASVDLGSDSF 120
Db 61 FAVDYTRKKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSINRASVDLGSDSF 120

QY 121 SQTSTGLVLAGVSYAVTPNVDDAGYRNYIGKVTYKKNVRSGLSAGYRVKF 174
Db 121 SQTSTGLVLAGVSYAVTPNVDDAGYRNYIGKVTYKKNVRSGLSAGYRVKF 174

RESULT 3

US-08-913-362-30
Sequence 30, Application US/08913362

Patent No. 6287574
GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis

APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500
CITY: Washington

STATE: D.C.
COUNTRY: USA

ZIP: 20007-5109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

TELEX: 904136
INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids

TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-913-362-30
Query Match 97.6%; Score 847.5; DB 4; Length 175;
Best Local Similarity 98.3%; Pred. No. 1.3e-89;

Matches 172; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MKKALATLIALPAALALAGAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALALAGAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRKKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSINRASVDLGSDSF 119
Db 61 FAVDYTRKKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSINRASVDLGSDSF 120

QY 120 SQTSTGLVLAGVSYAVTPNVDDAGYRNYIGKVTYKKNVRSGLSAGYRVKF 174
Db 120 SQTSTGLVLAGVSYAVTPNVDDAGYRNYIGKVTYKKNVRSGLSAGYRVKF 174

Db 121 FSQSTGLGVLAGVSYAVTPNVDDAGRYRYNIGKVTNKNVRSGLSAGVRKF 175

RESULT 4
US-08-913-362-4

; Sequence 4, Application US/08913362
; Patent No. 6287574

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

APPLICANT: Martin, Denis

APPLICANT: Hamel, Josee

APPLICANT: Rioux, Clement

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 175 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-913-362-4

Query Match 96.6%; Score 838.5; DB 4; Length 175;

Best Local Similarity 97.1%; Pred. No. 1.4e-88;

Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAHAKASSLSGAKGSPRISAGYRINDLR 60

Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAHAKASSLSGAKGSPRISAGYRINDLR 60

Db 1 FAVDYTRKKNK-APSTDFKLYSGASAIYDFDQSPVKPYLGARLSLNRAVDLGGSDS 119

Db 1 FAVDYTRKKNK-APSTDFKLYSGASAIYDFDQSPVKPYLGARLSLNRAVDLGGSDS 119

Db 61 FAVDYTRKKNK-APSTDFKLYSGASAIYDFDQSPVKPYLGARLSLNRAVDLGGSDS 120

Db 120 FSQSTGLGVLAGVSYAVTPNVDDAGRYRYNIGKVTNKNVRSGLSAGVRKF 174

Db 121 FSQSTGLGVLAGVSYAVTPNVDDAGRYRYNIGKVTNKNVRSGLSAGVRKF 175

RESULT 5

US-08-913-362-8

; Sequence 8, Application US/08913362

; Patent No. 6287574

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

APPLICANT: Martin, Denis

APPLICANT: Hamel, Josee

APPLICANT: Rioux, Clement

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-913-362-8

Query Match 96.1%; Score 834; DB 4; Length 174;

Best Local Similarity 95.4%; Pred. No. 4.5e-88;

Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAHAKASSLSGAKGSPRISAGYRINDLR 60

Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAHAKASSLSGAKGSPRISAGYRINDLR 60

Db 61 FAVDYTRKKNK-APSTDFKLYSGASAIYDFDQSPVKPYLGARLSLNRAVDLGGSDS 120

Db 61 FAVDYTRKKNK-APSTDFKLYSGASAIYDFDQSPVKPYLGARLSLNRAVDLGGSDS 120

Db 121 FSQSTGLGVLAGVSYAVTPNVDDAGRYRYNIGKVTNKNVRSGLSAGVRKF 174

Db 121 FSQSTGLGVLAGVSYAVTPNVDDAGRYRYNIGKVTNKNVRSGLSAGVRKF 174

RESULT 6

US-08-127-499A-20

; Sequence 20, Application US/08127499A

; Patent No. 5510264

GENERAL INFORMATION:

APPLICANT: VAN ALSTYNE, Diane

APPLICANT: SHARMA, Lawrence Rajendra

TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED

TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
STRAIN: 608B
US-08-913-362-26

Query Match 15.3%; Score 133; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.8e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
DB 1 FAVDYTRYKNYKAPSTDFKLYSIGA 25

RESULT 9
US-08-457-997B-2
Sequence 2, Application US/08457997B
Patent No. 576608
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,997B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gollick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-457-997B-2

Query Match 10.7%; Score 93; DB 1; Length 359;
Best Local Similarity 23.6%; Pred. No. 0.017;
Matches 54; Conservative 28; Mismatches 83; Indels 64; Gaps 11;

QY 1 MKKALATLIALAPAAALAEGA---SGFYVOADAA---HAKASSISGSAKGFSPRISAG 53
DB 1 MKKTAIALVAVAGLAASVAQAAPQENFTYAGYKAGGSGFHGGINNKAIGKISS--NYG 59
QY 54 YRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASAIYDFD-----TQSPVKPYL-----G 102

DB 60 YRNTFTTYGV-----FGYQILNOD---NFGLAELGYDDFGRAKLRAGKPRKAKHTNHG 111
QY 103 ARSLNRASVDLGSDSFSQSTGTL-----GVLA-GVS 134
DB 112 AYLSLKGSYEVLDGLDYGKAGVALVRSDYKREDFANGTRDHRKGRHTRASGLFVAGAE 171
QY 135 YATVPNDLDAGY-----RYNTIGKVTYKNVRS--GELSAGYRVKF 174
DB 172 YAVLPDLAVLEQWLTFRVGYKRPQDKPNTAIVNPMWICINAGISYRF 220

RESULT 10
US-08-467-722A-2
Sequence 2, Application US/08467722A
Patent No. 6030626
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,722A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gollick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-722A-2

Query Match 10.7%; Score 93; DB 3; Length 359;
Best Local Similarity 23.6%; Pred. No. 0.017;
Matches 54; Conservative 28; Mismatches 83; Indels 64; Gaps 11;

QY 1 MKKALATLIALAPAAALAEGA---SGFYVOADAA---HAKASSISGSAKGFSPRISAG 53
DB 1 MKKTAIALVAVAGLAASVAQAAPQENFTYAGYKAGGSGFHGGINNKAIGKISS--NYG 59
QY 54 YRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASAIYDFD-----TQSPVKPYL-----G 102
DB 60 YRNTFTTYGV-----FGYQILNOD---NFGLAELGYDDFGRAKLRAGKPRKAKHTNHG 111
QY 103 ARSLNRASVDLGSDSFSQSTGTL-----GVLA-GVS 134
DB 112 AYLSLKGSYEVLDGLDYGKAGVALVRSDYKREDFANGTRDHRKGRHTRASGLFVAGAE 171
QY 135 YATVPNDLDAGY-----RYNTIGKVTYKNVRS--GELSAGYRVKF 174
DB 172 YAVLPDLAVLEQWLTFRVGYKRPQDKPNTAIVNPMWICINAGISYRF 220

RESULT 11

```

1      MEDIUM TYPE: Floppy disk
2      COMPUTER: IBM PC compatible
3      OPERATING SYSTEM: PC-DOS/MS-DOS
4      SOFTWARE: Patentin Release #1.0, Version #1.30
5      CURRENT APPLICATION DATA:
6      APPLICATION NUMBER: US/08/913,362
7      FILING DATE: 13-NOV-1997
8      PRIOR APPLICATION DATA:
9      APPLICATION NUMBER: US 08/406,362
10     FILING DATE: 17-MAR-1995
11     PRIOR APPLICATION DATA:
12     APPLICATION NUMBER: US 60/001,983
13     FILING DATE: 04-AUG-1995
14     ATTORNEY/AGENT INFORMATION:
15     NAME: Bent, Stephen A.
16     REGISTRATION NUMBER: 29,768
17     REFERENCE/DOCKET NUMBER: 04/7998/0128
18     TELECOMMUNICATION INFORMATION:
19     TELEPHONE: (202)672-5300
20     TELEFAX: (202)672-5399
21     TELEX: 904136
22     INFORMATION FOR SEQ ID NO: 15:
23     SEQUENCE CHARACTERISTICS:
24     LENGTH: 16 amino acids
25     TYPE: amino acid
26     TOPOLOGY: linear
27     MOLECULE TYPE: protein
28     ORIGINAL SOURCE:
29     ORGANISM: Neisseria meningitidis
30     STRAIN: 608B
31     US-08-913-362-15
32
33     Query Match          10.0%; Score 87; DB 4; Length 16;
34     Best Local Similarity 100.0%; Pred. NO. 0.00077;
35     Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0
36
37     Oy      61 FAVDYTRYKNYKAPST 76
38             |||||||||||||||
39     Db      1 FAVDYTRYKNYKAPST 16
40
41 RESULT 13
42 US-08-733-230-6
43 ; Sequence 6, Application US/08733230
44 ; Patent No. 6025338
45 ; GENERAL INFORMATION:
46 ; APPLICANT: Barbet, Anthony F.
47 ; APPLICANT: Ganta, Roman Reddy
48 ; APPLICANT: McGuire, Travis C.
49 ; APPLICANT: Burridge, Michael J.
50 ; APPLICANT: Nyika, Aceme
51 ; APPLICANT: Rurangirwa, Fred R.
52 ; APPLICANT: Mahan, Sunan M.
53 ; TITLE OF INVENTION: Nucleic Acid Vaccines Against
54 ; TITLE OF INVENTION: Rickettsial Diseases and Methods of Use
55 ; NUMBER OF SEQUENCES: 6
56 ; CORRESPONDENCE ADDRESS:
57 ; ADDRESSEE: Saliwanchik & Saliwanchik
58 ; STREET: 2421 N.W. 41st Street, Suite A-1
59 ; CITY: Gainesville
60 ; STATE: FL
61 ; COUNTRY: USA
62 ; ZIP: 32606
63 ; COMPUTER READABLE FORM:
64 ; MEDIUM TYPE: Floppy disk
65 ; COMPUTER: IBM PC compatible
66 ; OPERATING SYSTEM: PC-DOS/MS-DOS
67 ; SOFTWARE: Patentin Release #1.0, Version #1.30
68 ; CURRENT APPLICATION DATA:
69 ; APPLICATION NUMBER: US/08/733,230
70 ; FILING DATE:
71 ; CLASSIFICATION: 514
72 ; ATTORNEY/AGENT INFORMATION:

```

NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF-167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-733-230-6

Query Match 9.4%; Score 81.5; DB 3; Length 282;
Best Local Similarity 25.2%; Pred. No. 0.24;
Matches 52; Conservative 22; Mismatches 75; Indels 57; Gaps 12;

QY 3 KALATLIALPAAALAE-----ASGYVQADAAHAKASSLGASGSPRISAGYRIN 57
DB 80 KSIAT-IDVSPANFSKSGYTFAPSKMLITSFDGA---VGSISGAR---VELEASYSR-- 130
QY 58 DLRA-----VDYTRKNYKAPSTDEKLYSIGASAIYD-PTQS 95
DB 131 --REATLADGOYAKSGAESLAIATRDANITETNYFVKKIDELITNSVLMNGCDVLTDL 188
QY 96 PVKPYLGARLSNRAVDLGSDSFSQSTGLGV--LAGSVAVTPNVLDAG----- 146
DB 189 FVSPYVCA--GIGASFPYDIS---KQVTKLAVRKRGVIGISYQFTPEISLVAGGFYHGLF 241
QY 147 -YRYNYGKAVYKAVRSGELSLAGVR 171
DB 242 DESYKDIPAHNSVK--FSGEAKKASVK 265

RESULT 14
US-08-953-326-6
Sequence 6, Application US/08953326
Patent No. 6251872
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: McGuire, Travis C.
APPLICANT: Butridge, Michael J.
APPLICANT: Nyika, Aceme
APPLICANT: Rurangirwa, Fred R.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
FILE REFERENCE: UF-167C1
CURRENT APPLICATION NUMBER: US/08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/733,230
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 282
TYPE: PRT
ORGANISM: Anaplasma marginale
US-08-953-326-6

Query Match 9.4%; Score 81.5; DB 4; Length 282;
Best Local Similarity 25.2%; Pred. No. 0.24;
Matches 52; Conservative 22; Mismatches 75; Indels 57; Gaps 12;
QY 3 KALATLIALPAAALAE-----ASGYVQADAAHAKASSLGASGSPRISAGYRIN 57
DB 80 KSIAT-IDVSPANFSKSGYTFAPSKMLITSFDGA---VGSISGAR---VELEASYSR-- 130
QY 58 DLRA-----VDYTRKNYKAPSTDEKLYSIGASAIYD-PTQS 95

DB 131 --REATLADGOYAKSGAESLAIATRDANITETNYFVKKIDELITNSVLMNGCDVLTDL 188
QY 96 PVKPYLGARLSNRAVDLGSDSFSQSTGLGV--LAGSVAVTPNVLDAG----- 146
DB 189 FVSPYVCA--GIGASFPYDIS---KQVTKLAVRKRGVIGISYQFTPEISLVAGGFYHGLF 241
QY 147 -YRYNYGKAVYKAVRSGELSLAGVR 171
DB 242 DESYKDIPAHNSVK--FSGEAKKASVK 265

RESULT 15
US-08-913-362-23
Sequence 23, Application US/08913362
Patent No. 6287574
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R.
APPLICANT: Martin, Denis
APPLICANT: Hamel, Joseph
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
STRAIN: 6088
US-08-913-362-23

Query Match 9.3%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 141 VDDAGYRYNYGKV 155
DB 1 VDDAGYRYNYGKV 15

Tue Oct 29 09:23:17 2002

us-09-684-883-6.rail

Page 8

Search completed: October 28, 2002, 16:04:20
Job time : 10.4864 secs

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a/accession: 0011/4
A/Status: preliminary

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A:Molecule type: DNA
 A:Residues: 1-174 <TEXT>
 A:Cross-references: GB:AE002420; GB:AE002098; NID:g7225876; PID:AA41081.1; PID:g722588
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB063

Query Match 98.8%; Score 858; DB 2; Length 174;
 Best Local Similarity 98.9%; Pred. No. 2,2e-68;
 Matches 172; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKRYKAPSTDFLTYSIGASATDEPTOSPYRYLGARLSLRASVDLGSSDSF 120
 DB 61 FAVDYTRYKRYKAPSTDFLTYSIGASATDEPTOSPYRYLGARLSLRASVDLGSSDSF 120
 QY 121 SQTSTGLVAGSYAVTPNVDLAGRYRYNIGKVTYVNVRSGLSAGRYK 174
 DB 121 SQTSTGLVAGSYAVTPNVDLAGRYRYNIGKVTYVNVRSGLSAGRYK 174

RESULT 3

opacit protein opak precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
 S16610
 N:Alternate names: outer membrane protein opak
 C:Species: Neisseria gonorrhoeae
 A:Variety: strain MS11
 C:Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
 C:Accession: S16610
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, M.; Microbiol. 5, 1889-1901, 1991
 A:Title: The opacit proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam
 A:Reference number: S16610; MUID:92114767
 A:Accession: S16610
 A:Molecule type: DNA
 A:Residues: 1-261 <BHA>
 A:Cross-references: EMBL:X52364
 A:Experimental source: strain MS11, variant 4.8
 A:Note: the authors did not translate the sequence for the signal peptide
 A:Note: expression of opacit proteins is regulated by the number of translated repeat
 A:Note: place the start codon in frame with the rest of the protein
 C:Genetics:
 A:Gene: opak
 C:Superfamily: opacit protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-261/Product: opacit protein opak #status predicted <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-75/Domain: extracellular #status predicted <EXT1>
 F:51-61/Region: semivariable region
 F:76-84/Domain: transmembrane #status predicted <TM2>
 F:89-95/Domain: transmembrane #status predicted <TM2>
 F:96-134/Domain: extracellular #status predicted <EXT2>
 F:102-129/Region: hypervariable region HV1
 F:135-149/Domain: transmembrane #status predicted <TM4>
 F:155-165/Domain: transmembrane #status predicted <TM5>
 F:166-212/Domain: extracellular #status predicted <EXT3>
 F:171-218/Region: hypervariable region HV2
 F:213-225/Domain: transmembrane #status predicted <TM6>
 F:229-237/Domain: transmembrane #status predicted <TM7>
 F:238-252/Domain: extracellular #status predicted <EXT4>
 F:253-261/Domain: transmembrane #status predicted <TM8>

Query Match 28.1%; Score 243.5; DB 2; Length 261;
 Best Local Similarity 30.3%; Pred. No. 4,2e-14;
 Matches 74; Conservative 24; Mismatches 59; Indels 87; Gaps 10;

QY 15 AALAEAS-ASGFYVQADAAHAKA-----SSLSGAKG-----FSPT 50
 DB 21 AQAASBNGNGPYQADLAAERITHDYPEPTGAKKGTISTVSDYFNIRKHSHPV 80

QY 51 SAGYRINDLRFADVTRYKRY-----KAPSTDFK-----LYS 82
 DB 81 SVGDFEGWRIADYAVYRRKNNKYSVSIKELLRRKNGNRRDLEAENGCTFAVSS 140
 QY 83 IGASATYDPTOSPYRYLGARLSN--RASVD-----LGG-----116
 DB 141 LGLSAVYDFKLNDFKPYIGARVAGVHRHSIDSTKRTTEVTILHGPCTTPVYRKN 200
 QY 117 -----SDFSQSTGLVAGSYAVTPNVDLAGRYRYNIGKVTYVNVRSGLSAGY 170
 DB 201 QNAHRESDSIR--VGLGAVAGVIGIDITPMLTDAGRYRYMGRLENTR-FKTHEASLGV 257

RESULT 4

opacit protein opak precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
 S16611
 N:Alternate names: outer membrane protein opa58
 C:Species: Neisseria gonorrhoeae
 A:Variety: strain MS11
 C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 26-Aug-1999
 C:Accession: S16611; S36345; S28624
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.; EMBO J. 12, 641-650, 1993
 A:Title: Variable opacit (Opa) outer membrane proteins account for the cell tropisms
 A:Reference number: S36328; MUID:93178439
 A:Accession: S36345
 A:Molecule type: DNA
 A:Residues: 24-260 <RUP>
 A:Cross-references: EMBL:Z18937; NID:949333; PID:CAA79370.1; PID:9940799
 A:Experimental source: strain MS11, variant F3
 A:Note: expression of opacit proteins is regulated by the number of translated repea
 A:Note: place the start codon in frame with the rest of the protein
 C:Genetics:
 A:Gene: opak
 C:Superfamily: opacit protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-260/Product: opacit protein opak #status predicted <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-74/Domain: extracellular #status predicted <EXT1>
 F:51-60/Region: semivariable region
 F:75-83/Domain: transmembrane #status predicted <TM2>
 F:88-94/Domain: transmembrane #status predicted <TM3>
 F:95-133/Domain: extracellular #status predicted <EXT2>
 F:101-128/Region: hypervariable region HV1
 F:134-148/Domain: transmembrane #status predicted <TM4>
 F:154-164/Domain: transmembrane #status predicted <TM5>
 F:165-211/Domain: extracellular #status predicted <EXT3>
 F:212-224/Domain: hypervariable region HV2
 F:228-236/Domain: transmembrane #status predicted <TM6>
 F:237-251/Domain: extracellular #status predicted <EXT4>
 F:252-260/Domain: transmembrane #status predicted <TM8>

Query Match 27.8%; Score 241; DB 2; Length 260;
 Best Local Similarity 29.8%; Pred. No. 7e-14;

Matches 77; Conservative 25; Mismatches 68; Indels 88; Gaps 10;

QY 2 KKAATLALPAAALAE---ASGFYQADAAH-----KASSLSGAKGS- 47

DB 6 KKPSTLFLSSMAAGEDHGRGPYQADLAVAYEHTHDYDEPTGKAKISTVSD 65

QY 48 -----PRISAGYRINDLRFADVITYRK-----KAPSTDFK 79

DB 66 YFRNIRTHSHIPRVSGVDFGGMRIADYARYRKNNKYSVSIKELLRNKNGNRTRDK 125

QY 80 -----LYSIGASAIYDFPTQSPVKPYLGARLSLN--RASVD-----LG 115

DB 126 TENQNGTFHAYVSLGSAVYDFKLNKFKRYIGARVAYGVHRSIDSTKTTTEVTIILH 185

QY 116 G-----SDSFSQSTGTGLAGVAYAVTPNVDDAGYRNYVICKVN 156

DB 186 GPGTTPYVPGKNTODAHRESDSIR--VGLGAVAGVGDITPMLTLTDAGYRHYWGRLE 243

QY 157 TVKNVSGELSGAYRVK 174

DB 244 NTR-FKTHEASLGYRVK 260

RESULT 5

S16613

Opacity protein opab precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

C:Species: Neisseria gonorrhoeae

A:Variety: strain MS11

C>Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997

C:Accession: S16613

R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, Mol. Microbiol. 5, 1889-1901, 1991

A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats

A:Reference number: S16610; MUID:92114767

A:Accession: S16613

A:Molecule type: DNA

A:Residues: 1-338 <BHA>

A:Cross-references: EMBL:X52373

A:Experimental source: strain MS11, variant 4.8

A:Note: the authors did not translate the sequence for the signal peptide

C:Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein

C:Genetics:

A:Gene: opab

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-13,14-104/Domain: signal sequence (fragments) #status predicted <SIG>

F:105-338/Product: opacity protein opab #status predicted <MAT>

F:115-123/Domain: transmembrane #status predicted <TM1>

F:124-155/Domain: extracellular #status predicted <EXT1>

F:132-141/Region: semivariable region

F:156-164/Domain: transmembrane #status predicted <TM2>

F:169-175/Domain: transmembrane #status predicted <TM3>

F:176-212/Domain: extracellular #status predicted <EXT2>

F:182-207/Region: hypervariable region HV1

F:213-227/Domain: transmembrane #status predicted <TM4>

F:224-289/Domain: extracellular #status predicted <EXT3>

F:233-243/Domain: transmembrane #status predicted <TM5>

F:249-295/Region: hypervariable region HV2

F:290-302/Domain: transmembrane #status predicted <TM6>

F:306-314/Domain: transmembrane #status predicted <TM7>

F:315-329/Domain: extracellular #status predicted <EXT4>

F:330-338/Domain: transmembrane #status predicted <TM8>

Query Match 27.7%; Score 240.5; DB 2; Length 338;

Best Local Similarity 30.5%; Pred. No. 1e-13;

Matches 74; Conservative 23; Mismatches 67; Indels 79; Gaps 9;

QY 10 ALALPAAALAE---ASGFYQADAAH-----KASSLSG-----AKGF 46

DB 97 SLFLPAAASGNGRGYQADLAVAYEHTHDYDEPTGAKKKKSTVDFYFRNIRTHST 156

QY 47 SPRISAGYRINDLRFADVITYRK--NYKAPSTDFK-----L 80

DB 157 HPRVSVGYDFGGMRIADYARYRKNNKYSYDIKLENNKNNKRDLTENQNGTFHAY 216

QY 81 YSIGASAIYDFPTQSPVKPYLGARLSLN--RASVD-----LG----- 116

DB 217 SSLGLSVYDFKLNKFKRYIGARVAYGVHRSIDSTKTTTEVTIILH 276

QY 117 -----SDSFSQSTGTGLAGVAYAVTPNVDDAGYRNYVICKVN 171

DB 277 TVNAHNSNIRRVGLGAVAGVGDITPMLTLTDAGYRHYWGRLENT-RFKTHEASLGYR 335

QY 172 VKF 174

DB 336 YRF 338

RESULT 6

S16612

Opacity protein opab precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

C:Species: Neisseria gonorrhoeae

A:Variety: strain MS11

C>Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997

C:Accession: S16612

R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc Mol. Microbiol. 5, 1889-1901, 1991

A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats

A:Reference number: S16610; MUID:92114767

A:Accession: S16612

A:Molecule type: DNA

A:Residues: 1-258 <BHA>

A:Cross-references: EMBL:X52369

A:Experimental source: strain MS11, variant 4.8

A:Note: the authors did not translate the sequence for the signal peptide

C:Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein

C:Genetics:

A:Gene: opab

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>

F:124-258/Product: opacity protein opab #status predicted <MAT>

F:134-42/Domain: transmembrane #status predicted <TM1>

F:143-74/Domain: extracellular #status predicted <EXT1>

F:50-60/Region: semivariable region

F:75-83/Domain: transmembrane #status predicted <TM2>

F:95-131/Domain: extracellular #status predicted <EXT2>

F:101-125/Region: hypervariable region HV1

F:132-146/Domain: transmembrane #status predicted <TM4>

F:152-162/Domain: transmembrane #status predicted <TM5>

F:163-209/Domain: extracellular #status predicted <EXT3>

F:168-215/Region: hypervariable region HV2

F:210-222/Domain: transmembrane #status predicted <TM6>

F:226-234/Domain: transmembrane #status predicted <TM7>

F:235-249/Domain: extracellular #status predicted <EXT4>

F:250-258/Domain: transmembrane #status predicted <TM8>

Query Match 27.6%; Score 240; DB 2; Length 258;

Best Local Similarity 30.1%; Pred. No. 8.5e-14;

Matches 77; Conservative 24; Mismatches 65; Indels 86; Gaps 10;

QY 2 KKAATLALPAAALAE---ASGFYQADAAH-----KASSLSGAK----- 44

DB 6 KKPSTLFLSSMAAGEDHGRGPYQADLAVAYEHTHDYDEPTGKAKISTVSD 65

QY 45 -----GFSRISAGYRINDLRFADVITYRK--NYKAPSTDFK----- 79

DB 66 YFRNIRTHSHIPRVSGVDFGGMRIADYARYRKNNKYSVSIKELLRNKNGNRTRDK 125

QY 80 -----LYSIGASAIYDFPTQSPVKPYLGARLSLN--RASVD-----LG- 116

DB 126 NOENGTFAVSSLSGSAVYDFKLNKFKRYIGARVAYGVHRSIDSTKTTTEVTIILHG 185

17 ALAAGSGFYVQADAAH-----KASSSLG-----AKGSPRISAGY 54
1 ASDEGGGPGYVQADLAAYEHITHDYPEPTAPKMKISTVSDYFNIRTRSPVSVG 60
55 RINDLRFAVDTYRKYN-----KAPSDFK-----LVSIGAS 86
61 DFGGWRIAADYARYRRKNNKYSVSIKELLRNKNGNRIDLKRNQENGTFFHVASLSGLS 120
87 AITDFTQSPVRYLGAARSLN--RASVD-----LGG----- 116
121 AYVDFKLNDFKFKYIGARVAVGHVRSIDSTKTKTEVTTLHGPGTTPVYDGKNQDAH 180
117 --SDSFQSTGTGLVAGSYAATPVNDLADGRYNTICKVNTKAVNGEISAGYRVK 174
181 RESDSIR--VGLGAVAGVIDITPMLTDAGRYHYHGLENT-RFKTHASLGVRYR 237

RESULT 9

S16614

Opacity protein opaf precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

C:Species: Neisseria gonorrhoeae

A:Variety: strain MS11

C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997

C:Accession: S16614

R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehmig, F.; Stern, A.; Kupsch, Mol. Microbiol. 5, 1889-1901, 1991

A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam

A:Reference number: S16610; MUID:92114767

A:Accession: S16614

A:Molecule type: DNA

A:Residues: 1-257 <BHA>

A:Cross-references: EMBL:X52368

A:Experimental source: strain MS11, variant 4.8

A>Note: the authors translated the codon ACC for residue 206 as Ala and TAT for residue

A>Note: the authors did not translate the sequence for the signal peptide

A>Note: expression of opacity proteins is regulated by the number of translated repeat e

C:Genetics: of repeats place the start codon in frame with the rest of the protein

A:Gene: opaf

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>

F:24-257/Product: opacity protein opaf #status predicted <MAT>

F:34-42/Domain: transmembrane #status predicted <TM1>

F:43-74/Domain: extracellular #status predicted <EXT1>

F:51-60/Region: semivariable region

F:75-83/Domain: transmembrane #status predicted <TM2>

F:88-94/Domain: transmembrane #status predicted <TM3>

F:95-131/Domain: extracellular #status predicted <EXT2>

F:101-126/Region: hypervariable region HV1

F:132-146/Domain: transmembrane #status predicted <TM4>

F:153-162/Domain: transmembrane #status predicted <TM5>

F:163-208/Domain: extracellular #status predicted <EXT3>

F:168-214/Region: hypervariable region HV2

F:209-221/Domain: transmembrane #status predicted <TM6>

F:223-233/Domain: transmembrane #status predicted <TM7>

F:234-248/Domain: extracellular #status predicted <EXT4>

F:249-257/Domain: transmembrane #status predicted <TM8>

Query Match 27.6%; Score 239.5; DB 2; Length 257;

Best local Similarity 29.6%; Pred. No. 9.3e-14; Indels 81; Gaps 9;

Matches 75; Conservative 24; Mismatches 73;

2 KKAATLIALALPAALAE--ASGFYVQADAAH-----KASSSLGSK----- 44

6 KKPILLFSSLLFSSAAQAGDHGRGPYVQADLAAYEHITHDYPEPTGTTKDKISTVSD 65

45 -----GSPRISAGYRINDLRFAVDYTRYK--NYKAPSTDK----- 79

66 YFNIRTHSHIPRVSVDGFGMRIDYARYRRKNNKYSVDIKELNNKNNKNDLAKTE 125

80 -----LVSIGASAIYDDTQSPVRYLGAARSLN--RASVD-----LGG 116

126 NQENGTFFHVASLSGLSAVYDFKLNDFKPKYIGARVAVGHVRSIDSTKTKTKELTSSYG 185
117 -----SDSFQSTGTGLVAGSYAATPVNDLADGRYNTICKVNTKAVNGEISAGYRVK 161
186 LNPVYTEENTQMAHQNSIRRVGLVYAGVGIDITPKLTDGRYHYHGLENT-R 244
162 RSGELAGYRVK 174
245 KTHASLGVRYR 257

RESULT 10

S16616

Opacity protein opaf precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

C:Species: Neisseria gonorrhoeae

A:Variety: strain MS11

C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997

C:Accession: S16616

R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehmig, F.; Stern, A.; Kupsc

Mol. Microbiol. 5, 1889-1901, 1991

A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f

A:Reference number: S16610; MUID:92114767

A:Accession: S16616

A:Molecule type: DNA

A:Residues: 1-266 <BHA>

A:Cross-references: EMBL:X52372

A:Experimental source: strain MS11, variant 4.8

A>Note: the authors did not translate the sequence for the signal peptide

A>Note: expression of opacity proteins is regulated by the number of translated repea

C:Genetics: of repeats place the start codon in frame with the rest of the protein

A:Gene: opaf

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>

F:24-266/Product: opacity protein opaf #status predicted <MAT>

F:34-42/Domain: transmembrane #status predicted <TM1>

F:43-74/Domain: extracellular #status predicted <EXT1>

F:51-60/Region: semivariable region

F:75-83/Domain: transmembrane #status predicted <TM2>

F:88-94/Domain: transmembrane #status predicted <TM3>

F:95-131/Domain: extracellular #status predicted <EXT2>

F:101-134/Region: hypervariable region HV1

F:140-154/Domain: transmembrane #status predicted <TM4>

F:160-170/Domain: transmembrane #status predicted <TM5>

F:171-217/Domain: extracellular #status predicted <EXT3>

F:176-223/Region: hypervariable region HV2

F:218-230/Domain: transmembrane #status predicted <TM6>

F:224-242/Domain: transmembrane #status predicted <TM7>

F:243-257/Domain: extracellular #status predicted <EXT4>

F:258-266/Domain: transmembrane #status predicted <TM8>

Query Match 27.4%; Score 238; DB 2; Length 266;

Best local Similarity 29.4%; Pred. No. 1.3e-13; Indels 90; Gaps 8;

Matches 77; Conservative 24; Mismatches 71;

2 KKAATLIALALPAALAE--ASGFYVQADAAH-----KASSSLG----- 42

6 KKPILLFSSLLFSSAAQAGDHGRGPYVQADLAAYEHITHDYPEPTGTTKDKISTVSD 65

43 -----AKGSPRISAGYRINDLRFAVDYTRYK----- 69

66 YFNIRTHSHIPRVSVDGFGMRIDYARYRRKNNKYSVDIKELNNKNNKNDLAKTE 125

70 NYKAPSTDK-----LVSIGASAIYDDTQSPVRYLGAARSLN----- 107

126 NIKTRKTRHRENTFFHVASLSGLSAVYDDTQSPVRYLGAARSLN----- 185

108 -----NRASV-----DLGSDSFQSTGTGLVAGSYAATPVNDLADGRYRVYI 152

186 AVTYTPQNAASVTYNAPTRKLPHEHSRISISLGGAVAGVIDITPMLTDAGRYRNM 245

153 GKVNIVKAVNRSGELAGYRVK 174

Db 246 GRLEWTR-FKTHEASLGRYRF 266

RESULT 11

opacity protein-related protein OPM1 precursor - Neisseria meningitidis (strain C1938)

N:Alternate names: outer membrane protein class 5

C:Species: Neisseria meningitidis

A:Variety: strain C1938

C:Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 20-Jun-2000

C:Accession: S08514

R:Stem, A: Meyer, T.F.

Mol. Microbiol. 1, 5-12, 1987

A:Title: Common mechanism controlling phase and antigenic variation in pathogenic neisseria

A:Reference number: S08513; MUID:88260884

A:Accession: S08514

A:Molecule type: DNA

A:Residues: 1-258 <STB>

A:Cross-References: EMBL:X06445; NID:q44906; PID:g1333787

A:Note: expression of opacity proteins is regulated by the number of translated repeat

of repeats place the start codon in frame with the rest of the protein

C:Genetics:

A:Gene: opr1

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-13/14-21/Domain: signal sequence (fragments) #status predicted <SIG>

F:22-258/Product: opacity protein-related protein OPM1 #status predicted <MAT>

F:33-41/Domain: transmembrane #status predicted <TM1>

F:42-73/Domain: extracellular #status predicted <EXT1>

F:50-59/Region: semivariable region

F:74-82/Domain: transmembrane #status predicted <TM2>

F:87-93/Domain: transmembrane #status predicted <TM2>

F:94-129/Domain: extracellular #status predicted <EXT2>

F:100-124/Region: hypervariable region HV1

F:130-144/Domain: transmembrane #status predicted <TM4>

F:150-160/Domain: transmembrane #status predicted <TM5>

F:161-209/Domain: extracellular #status predicted <EXT3>

F:166-215/Region: hypervariable region HV2

F:210-222/Domain: transmembrane #status predicted <TM6>

F:226-234/Domain: transmembrane #status predicted <TM7>

F:235-249/Domain: extracellular #status predicted <EXT4>

F:250-258/Domain: transmembrane #status predicted <TM8>

Query Match 27.3%; Score 237; DB 2; Length 258;

Best Local Similarity 28.9%; Pred. No. 1.6e-13;

Matches 71; Conservativity 27; Mismatches 68; Indels 80; Gaps 7;

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QY 8 LIALALPAALALGASGFYVQADAAH-----KASSSLG-----AKG 45
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 14 LFSSAAQAASSEDGSRSPYVQADLAFAERITHNYDEPTGADKISTVSDYFRNIRAH 73
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 46 FSPRISAGRIINDLRFAVDYTRYK-----NYKAPSTDFK-----L 80
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 74 IHRVAVGVDFGGRWIAADYASRKWKESNFKYTEIKDKYKTEKEHOGNSFHA 133
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 81 YSICASAIYDFDTQSPVKPYGLARLSLN-----ASVDLGS----- 117
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 134 SSIGLSAIYDFDKNDKFKYIGARVAHYVHKHVSVEKTTTTSKPGGTPAGGPV 193
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 118 -----DSFSQTSTGLGAGVSYAVTPNVDLAGRYNIGKVNIVKVRSGELSA 168
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 194 TDPSPKPYHSHSISISIGLGVAGVGFDTIPKLLDTGTGRYHNGRLEWTR-FK 252
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 169 GVRVKE 174
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 253 GMKRRF 258
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 12

opacity protein B precursor (clone pFLOB1700) - Neisseria meningitidis (strain FAM18) (F

N:Alternate names: outer membrane protein class 5

C:Species: Neisseria meningitidis

A:Variety: strain FAM18

C:Date: 04-Jun-1997 #sequence_revision 04-Jun-1997 #text_change 17-Oct-1997

C:Accession: S20043

R:Abho, E.L.; Dempsey, J.A.; Hobbs, M.M.; Klapper, D.G.; Cannon, J.G.

Mol. Microbiol. 5, 1429-1437, 1991

A:Title: Characterization of the opa (class 5) gene family of Neisseria meningitidis.

A:Reference number: S16286; MUID:92157869

A:Accession: S20043

A:Molecule type: DNA

A:Residues: 1-254 <AHO>

A:Cross-References: EMBL:X63108

A:Experimental source: strain FAM18; clone pFLOB1700

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991

A:Note: only a part of the translation is shown

A:Note: expression of opacity proteins is regulated by the number of translated repeat

of repeats place the start codon in frame with the rest of the protein

C:Genetics:

A:Gene: opab

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-19/Domain: signal sequence (fragment) #status predicted <SIG>

F:20-254/Product: opacity protein OPAB #status predicted <MAT>

F:31-39/Domain: transmembrane #status predicted <TM1>

F:40-69/Domain: extracellular #status predicted <EXT1>

F:70-78/Domain: transmembrane #status predicted <TM2>

F:89-99/Domain: transmembrane #status predicted <TM3>

F:90-126/Domain: extracellular #status predicted <EXT2>

F:127-141/Region: hypervariable region HV1

F:147-157/Domain: transmembrane #status predicted <TM4>

F:158-205/Domain: extracellular #status predicted <EXT3>

F:163-211/Region: hypervariable region HV2

F:206-218/Domain: transmembrane #status predicted <TM6>

F:222-230/Domain: transmembrane #status predicted <TM7>

F:231-245/Domain: extracellular #status predicted <EXT4>

F:246-254/Domain: transmembrane #status predicted <TM8>

Query Match 27.2%; Score 236; DB 2; Length 254;

Best Local Similarity 28.7%; Pred. No. 1.9e-13;

Matches 70; Conservativity 29; Mismatches 67; Indels 78; Gaps 7;

```

QY 8 LIALALPAALALGASGFYVQADAAH-----KASSSLG-----AKGS 47
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 12 LFSSAAQAASSEDGSRSPYVQADLAFAERITHDYPRKATGANNSTVSDYFRNIRAH 71
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 48 PRISAGRIINDLRFAVDYTRYKN-----KAPSTDFKLY 81
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 72 PRVAVGVDFGGRWIAADYASRKNNNNKYSVNTKELENKNNKKDKLTENGQGTFFHA 131
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 82 SIGASAIYDFDTQSPVKPYGLARLSLN-----RASVDL-----GSD 118
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 132 SSIGLSAIYDFDKNDKFKYIGARVAHYVHSHSIDSTKTEVYTLTHGADTPRTYNGE 191
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 119 -----DSFSQTSTGLGAGVSYAVTPNVDLAGRYNIGKVNIVKVRSGELSA 170
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 192 STONAVHSHSIRRLGAGVAGVGFDTIPKLLDTGTGRYHNGRLEWTR-FK 250
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 171 RVKF 174
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 251 RYHF 254
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 13

opacity protein P.II precursor - Neisseria gonorrhoeae (strain F62-SF and others) (F

C:Species: Neisseria gonorrhoeae

A:Variety: strain F62-SF

C:Date: 30-Jun-1991 #sequence_revision 17-Oct-1997 #text_change 13-Nov-1998

C:Accession: S04380; S16504

R:Palmer, L.; Brooks, G.F.; Falkow, S.

MOL. Microbiol. 3, 663-671, 1989
 A:Title: Expression of gonococcal protein II in *Escherichia coli* by translational fusion
 A:Reference number: S04380; MUID:89343653
 A:Accession: S04380
 A:Molecule type: DNA
 A:Residues: 1-270 <PAL>
 A:Cross-references: EMBL:X15780
 A:Experimental source: Strain F62-SF, serogroup IB-3; clone F62-SF1
 A>Note: the authors did not translate the sequence of the signal peptide
 A>Note: expression of opacity proteins is regulated by the number of translated repeat
 R:aha, M.K.; So, M.; Seifert, H.S.; Bilyard, E.; Marchal, C.
 EMO J. 7, 4367-4378, 1988
 A:Title: Pilin expression in *Neisseria gonorrhoeae* is under both positive and negative t
 A:Reference number: S02017; MUID:89210824
 A:Accession: S16504
 A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 259-270 <TAH>
 A:Cross-references: EMBL:X13965
 A:Experimental source: strain MS11A
 A>Note: expression of opacity proteins is regulated by the number of translated repeat
 C: repeats place the start codon in frame with the rest of the protein
 C:Genetics:
 A:Gene: opa1
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-270/Product: opacity protein opa #status predicted <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-75/Domain: extracellular #status predicted <EXT1>
 F:51-61/Region: semivariable region
 F:76-84/Domain: transmembrane #status predicted <TM2>
 F:89-95/Domain: transmembrane #status predicted <TM3>
 F:96-141/Domain: extracellular #status predicted <EXT2>
 F:102-136/Region: hypervariable region HV1
 F:142-156/Domain: transmembrane #status predicted <TM4>
 F:162-172/Domain: transmembrane #status predicted <TM5>
 F:173-221/Domain: extracellular #status predicted <EXT3>
 F:178-227/Region: hypervariable region HV2
 F:222-234/Domain: transmembrane #status predicted <TM6>
 F:238-246/Domain: transmembrane #status predicted <TM7>
 F:247-261/Domain: extracellular #status predicted <EXT4>
 F:262-270/Domain: transmembrane #status predicted <TM8>

Query Match 27.2%; Score 236; DB 2; Length 270;
 Best Local Similarity 27.4%; Pred. No. 2e-13;
 Matches 73; Conservative 31; Mismatches 68; Indels 94; Gaps 8;

2 KRALATLALPAALAEAG--ASGFYVADAAH-----AKASSLSGSAK 44
 6 KPSILFSSLSAQAAGBNGRPYQADLAAYEHITHDYKPKGAKKGTITSVS 65
 45 GF-----SPRISAGYRINDLFAVDYTRYK----- 69
 66 DFFNRIRHSHVPRVSVGDFGMRIDYARYRKMNKKYSVSIKELGRNDNSASGVRG 125
 70 --NYKAPSTDF-----LVSIGASATYDDPTGSPYKPYIGARLSL----- 107
 126 HNITOTTEHDENTFFAASSLSGLSTYDDTGSRRPYIGARVAVGHVHQVRSVEOE 185
 108 -----NRASVDLGG-----DSFSQSTGTGLAGVAVTPVNDAGYR 148
 186 TEIVTTPREKQNVAPSPRIGAPTKRPAHNEBSRISLSLGFCAVAGVGDITPTNLIDAGYR 245
 149 YNIGKVTAVNVRSGLSAGYRKF 174
 246 YHMGRLNTR-FKTHEASLGVRKF 270

RESULT 14
 K0NH2C
 opacity protein P.IIC precursor - *Neisseria gonorrhoeae* (strain JS3) (fragments)

N:Alternate names: outer membrane protein P.IIC
 C:Species: *Neisseria gonorrhoeae*
 A:Variety: Strain JS3
 C:Date: 31-Mar-1992 #sequence_revision 17-Oct-1997 #text_change 08-May-1998
 C:Accession: S03095; S16360
 R:van der Ley, P.
 MOL. Microbiol. 2, 797-806, 1988
 A:Title: Three copies of a single protein II-encoding sequence in the genome of *Neis*
 A:Reference number: S03095; MUID:89096501
 A:Accession: S03095
 A:Molecule type: DNA
 A:Residues: 1-268 <VAN>
 A:Cross-references: EMBL:X12625
 A:Experimental source: strain JS3
 A>Note: 241-val was also found
 A>Note: expression of opacity proteins is regulated by the number of translated repea
 R:Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
 Infect. Immun. 55, 2026-2031, 1987
 A:Title: Antigenic and structural differences among six proteins II expressed by a si
 A:Reference number: S16360; MUID:87306843
 A:Accession: S16360
 A>Status: Preliminary
 A:Molecule type: protein
 A:Residues: 24-34 <BAR>
 C:Genetics:
 A:Gene: piliC
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-268/Product: opacity protein P.IIC #status experimental <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-74/Domain: extracellular #status predicted <EXT1>
 F:51-60/Region: semivariable region
 F:75-83/Domain: transmembrane #status predicted <TM2>
 F:88-94/Domain: transmembrane #status predicted <TM3>
 F:95-140/Domain: extracellular #status predicted <EXT2>
 F:101-135/Region: hypervariable region HV1
 F:141-155/Domain: transmembrane #status predicted <TM4>
 F:161-171/Domain: transmembrane #status predicted <TM5>
 F:172-219/Domain: extracellular #status predicted <EXT3>
 F:177-225/Region: hypervariable region HV2
 F:220-232/Domain: transmembrane #status predicted <TM6>
 F:236-244/Domain: transmembrane #status predicted <TM7>
 F:245-259/Domain: extracellular #status predicted <EXT4>
 F:260-268/Domain: transmembrane #status predicted <TM8>

Query Match 27.1%; Score 235.5; DB 1; Length 268;
 Best Local Similarity 27.2%; Pred. No. 2e-13;
 Matches 70; Conservative 30; Mismatches 68; Indels 89; Gaps 8;

6 ATLIALALPAALAEAGSGFYVADAAHAKA-----SSLSGSAK----- 44
 13 SLSLSSAARASDGGRGPRYQADLAAYEAERTHDYKPKTGKKNISTVSDYFNIRT 72
 45 -GSPRISAGYRINDLFAVDYTRYK-----NYKAPS 75
 73 HSHVPRVSVGDFGSMRIDYARYRKMNKKYSVSIKELGRNDNSASGVRGHLNITOT 132
 76 TDFK-----LVSIGASATYDDPTGSPYKPYIGARLSLRA-----SYDL----- 114
 133 TEHDENTFFAASSLSGLSTYDDTGSRRPYIGMVAAGVHGHQVRSVEOEETITTPY 192
 115 --GGSDFSQ-----TSTGIGVLAVGSAVTPVNDAGYRNYIGKVT 157
 193 SNGGKVSLSKMPKPSAHNHSNIRRGVLGAVAGGFITRLTIDTGYRYHMGRLN 252
 158 YKAVRSGLSAGYRKF 174
 253 TR-FKTHEASLGVRKF 268

RESULT 15

S72343
 opacity protein opaH precursor - Neisseria gonorrhoeae (isolate 150636)
 N:Alternate names: cell invasion protein opaH
 C:Species: Neisseria gonorrhoeae
 A:Variety: isolate 150636
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
 C:Accession: S72343
 R:Waldreser, L.S.; Ajoka, R.S.; Merz, A.J.; Puaol, D.; Lin, L.; Thomas, M.; So, M.
 Mol. Microbiol. 13, 919-928, 1994
 A:Title: The opaH locus of Neisseria gonorrhoeae MS11a is involved in epithelial cell in
 A:Reference number: S72343; MUID:95115561
 A:Accession: S72343
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-283 <MAL>
 A:Cross-references: EMBL:U13708; NID:9535357; PIDN:AA74082.1; PID:9535358
 A:Experimental source: isolate 150636
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
 A:Note: expression of opacity proteins is regulated by the number of translated repeat
 of repeats place the start codon in frame with the rest of the protein
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-48/Domain: signal sequence #status predicted <SIG>
 F:49-283/Product: opacity protein opaH #status predicted <MAT>
 F:58-66/Domain: transmembrane #status predicted <TM1>
 F:67-98/Domain: extracellular #status predicted <EXT1>
 F:75-84/Region: semivariable region
 F:99-107/Domain: transmembrane #status predicted <TM2>
 F:112-118/Domain: transmembrane #status predicted <TM3>
 F:119-155/Domain: extracellular #status predicted <EXT2>
 F:125-150/Region: hypervariable region HV1
 F:156-170/Domain: transmembrane #status predicted <TM4>
 F:176-186/Domain: transmembrane #status predicted <TM5>
 F:187-234/Domain: extracellular #status predicted <EXT3>
 F:192-240/Region: hypervariable region HV2
 F:235-247/Domain: transmembrane #status predicted <TM6>
 F:251-259/Domain: transmembrane #status predicted <TM7>
 F:260-274/Domain: extracellular #status predicted <EXT4>
 F:275-283/Domain: transmembrane #status predicted <TM8>

Query Match 27.1% Score 235; DB 2; Length 283;
 Best Local Similarity 28.3%; Pred. No. 2.6e-13;
 Matches 69; Conservative 27; Mismatches 60; Indels 80; Gaps 7;

QY	10	ALALPAALAEAGASGFYVQADAHAKA-----SSLSGAKG-----FS 47
DB	41	SLLSAAQAASEAMRGVYQADLAFPAERTHDYPTGTGKCTISTVSDYFNIRTHSVH 100
QY	48	PRISAGYRINDLRFVADYTRKKNY-----KAPS-----TDFKLY 81
DB	101	PRYSVGYDYGWRRIADYARVYRKMNKNKYSVNIERYQEAHSNRIDLKAEQDENGTFHAYS 160
QY	82	STGASAIYDFDQSPYKPYLGARLSLN--RASVDL----- 114
DB	161	SLGLSNVYDFKLNDRKPYLGARVAVGHRHSIDSKTKTILTSFYGATKPTTYDIGP 220
QY	115	---GGSDFESQTSGLGYLAGVSAVTPNVDLAGYRYNYIGKVVYKAVNRSGLSAGV 170
DB	221	KQDAHQESNSIRYVGLGYLAGVGFDTPTKLTLDIGYRHYWGRLENTN-FTTHASISLM 279
QY	171	RYKF 174
DB	280	RYRF 283

Search completed: October 28, 2002, 16:03:36
 Job time : 13.4821 secs

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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:55:44 ; Search time 6.98996 Seconds

(without alignments)
963.840 Million cell updates/sec

Title: US-09-684-883-6

Perfect score: 868
Sequence: 1 MKKALATILIALALPAALAE.....VNTVKNVSGELSGAVRYKF 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	239.5	27.6	237	1	OPAK_NEIGO
2	238	27.4	260	1	OPRI_NEIMC
3	235.5	27.1	270	1	OPMC_NEIGO
4	234	27.0	236	1	OPAC_NEIGO
5	231.5	26.7	234	1	OPAB_NEIGO
6	231.5	26.7	237	1	OPAJ_NEIGO
7	231	26.6	234	1	OPAE_NEIGO
8	231	26.6	234	1	OPAF_NEIGO
9	230	26.5	233	1	OP67_NEIGO
10	225	25.9	234	1	OP28_NEIGO
11	225	25.9	234	1	OP65_NEIGO
12	225	25.9	238	1	OP66_NEIGO
13	225	25.9	238	1	OPAH_NEIGO
14	223.5	25.7	243	1	OPAD_NEIGO
15	223	25.7	244	1	OPAL_NEIGO
16	220	25.3	178	1	OP57_HAEIN
17	219	25.2	238	1	OP68_NEIGO
18	214	24.7	239	1	OPAA_NEIGO
19	205.5	23.7	247	1	OPAG_NEIGO
20	177.5	20.4	121	1	OPG_HAEIN
21	135	15.6	170	1	OPR3_NEIMC
22	122.5	14.1	70	1	VA14_HAEIN
23	113	13.0	182	1	ATL_TERPS
24	100	11.5	353	1	OM52_HAEIN
25	99	11.4	353	1	OM51_HAEIN
26	98.5	11.3	350	1	OMPA_SALTY
27	98	11.3	521	1	TSAS_RICHS
28	97	11.2	213	1	OM25_BRUBA
29	96	11.1	178	1	ATL_YEREN
30	96	11.1	212	1	OMFW_ECOLI
31	93.5	10.8	341	1	OMP7_VIBCH
32	93.5	10.8	428	1	OM47_PASBU
33	93	10.7	359	1	OM53_HAEIN

34	89	10.3	213	1	OM25_BRUSU	Q45689 brucella su
35	88.5	10.2	346	1	OMPA_ECOLI	P02934 escherichia
36	87	10.0	213	1	OM25_BRUME	Q45321 brucella me
37	87	10.0	349	1	OMPA_BUCAT	P57414 brucella ap
38	87	10.0	350	1	PORF_PSEAE	P13794 pseudomonas
39	84.5	9.7	995	1	Y109_YEAST	P40442 saccharomyc
40	84	9.7	511	1	INO1_ARATH	P42801 arabidopsis
41	84	9.7	511	1	INO1_PHAVU	Q41107 phaseolus v
42	83.5	9.6	350	1	OMPA_ENDAE	P09146 enterobacte
43	83	9.6	201	1	OM25_BRNOV	Q45335 brucella ov
44	83	9.6	213	1	OM25_BRUCA	Q45110 brucella ca
45	82	9.4	172	1	OMP7_ENTCL	P25253 enterobacte

ALIGNMENTS

RESULT 1	OPAK_NEIGO	STANDARD;	PRT;	237 AA.
ID	OPAK_NEIGO			
AC	Q04880;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	01-NOV-1995 (Rel. 32, Last annotation update)			
DE	Opacity protein OPA57 precursor (Fragment).			
GN	OPAK.			
OS	Neisseria gonorrhoeae.			
CC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			
OX	NCBI_TaxID:485;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MS11 / F3;			
RX	MEDLINE=93178439; Pubmed=8440254;			
RA	Kirsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;			
RT	"Variable opacity (Opa) outer membrane proteins account for the cell			
RT	envelopes displayed by Neisseria gonorrhoeae for human leukocytes and			
RT	epithelial cells."			
RL	EMBO J. 12:641-650(1993).			
CC	-!- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA			
CC	PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE			
CC	VARIATION.			
CC	-!- SUBCELLULAR LOCATION: Outer membrane.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	-----			
DR	EMBL; Z18935; CAA79368.1; -			
DR	PIR; S28626; S28626.			
DR	InterPro; IPR003394; Opacity.			
DR	Pfam; PF02462; Opacity; 1.			
KW	Outer membrane; Multigene family; Signal.			
FT	NON_TER	1		
FT	SIGNAL	<1		
FT	CHAIN	2	>237	POTENTIAL.
FT	NON_TER	237		OPACITY PROTEIN OPA57.
SO	SEQUENCE	237 AA;	26703 MW;	FBI1A0FB5C7EBCAD CRC64;
Query Match	27.6%;	Score 239.5;	DB 1;	Length 237;
Best local similarity	30.0%;	Pred. No. 1.6e-14;		
Matches	72;	Conservative 24;	Mismatches 59;	Indels 85; Gaps 9;
QY	17 ALAAGAGFVQADAAH-----KASSSLGS-----AKGFSPTISAGY 54			
DB	1 ASEGCGGPRVQADLAYAYEHITHDYPEPPAPKKNISVSDYFRNIRRSVHPVSQY 60			
QY	55 RINDLRPAVYTRKNV-----KAPSTDEK-----LVSIGNS 86			
DB	61 DFGWRIDADYATRKKNKNSYSIKELIRKNGNRTDLAENQENGTFAVSVSLGIS 120			

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QY 87 AYDFPDQSPVRYLGRSLN--RASVD-----LGG----- 116
DB 121 AYDFKLNKFKFYIGARVAVGHVHSIDSTKTEVTITLHGPGTTPVYDQKNTQAH 180
QY 117 -SDSFQSTGTGLGVLAVYATPVNDADAGRYNYICKVNTVKVNGSELGAGVRYKF 174
DB 181 RESDSIRH--VGLGAVAGVGIDITPMLTLDAGYRHYWGLHENTR--FKTHEASLGAVRYKF 237

RESULT 2
ID OMPC_NEIGO STANDARD: PRT: 260 AA.
AC P10170;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Opacity-related protein POPM1.
GN OPR.
OS Neisseria meningitidis (serogroup C).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=135720;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1938 / SEROGROUP C;
RX MEDLINE=88260884; PubMed=2455211;
RA Stern A., Meyer T.F.;
RT "Common mechanism controlling phase and antigenic variation in
RT pathogenic neisseriae."
RL Mol. Microbiol. 1:5-12(1987).
CC - SUBCELLULAR LOCATION: Outer membrane.
CC - SIMILARITY: STRONG TO THE OPACITY-RELATED PROTEIN POPM3 AND
CC REGIONS OF HOMOLOGY WITH N.GONORRHOEA (STRAIN MS11) OPA GENE
CC PRODUCTS.
CC -----
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CC -----
CC
CC EMBL: X06445; CAA29748.1; ALT_SEQ.
CC PIR: S08514; S08514.
CC InterPro: IPR003394; Opacity.
CC Pfam: PF02462; Opacity; 1.
CC Outer membrane.
CC KW
CC SEQUENCE 260 AA; 28936 MW; EB47A2843B3F037B CRC64;

Query Match 27.4%; Score 238; DB 1; Length 260;
Best Local Similarity 28.0%; Pred. No. 2.4e-14;
Matches 72; Conservative 32; Mismatches 67; Indels 86; Gaps 8;

```

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RESULT 3
ID OMPC_NEIGO STANDARD: PRT: 270 AA.
AC P09888;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Outer membrane protein P.IIC precursor (Protein IIC).
GN PIIC.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J53;
RX MEDLINE=89096501; PubMed=3145386;
RA van der Ley P.;
RT "Three copies of a single protein II-encoding sequence in the genome
RT of Neisseria gonorrhoeae J53: evidence for gene conversion and gene
RT duplication."
RL Mol. Microbiol. 2:797-806(1988).
CC - FUNCTION: THIS PROTEIN SERVES AS A PORIN.
CC - SUBUNIT: HOMOTRIMER.
CC - SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -----
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CC -----
CC
CC EMBL: X12625; CAA31144.1; -.
CC PIR: S03095; KONH2C.
CC InterPro: IPR003394; Opacity.
CC Pfam: PF02462; Opacity; 1.
CC Outer membrane; Porin; Transmembrane; Antigen; Signal.
CC KW
CC SIGNAL 1 25
CC CHAIN 26 270
CC TRANSMEM 36 44 OUTER MEMBRANE PROTEIN P. IIC.
CC TRANSMEM 77 85
CC TRANSMEM 90 96 POTENTIAL.
CC TRANSMEM 143 157 POTENTIAL.
CC TRANSMEM 163 173 POTENTIAL.
CC TRANSMEM 222 234 POTENTIAL.
CC TRANSMEM 238 246 POTENTIAL.
CC TRANSMEM 262 270 POTENTIAL.
CC SEQUENCE 270 AA; 30269 MW; FEB448373830A50D CRC64;

Query Match 27.1%; Score 235.5; DB 1; Length 270;
Best Local Similarity 27.2%; Pred. No. 4.2e-14;
Matches 70; Conservative 30; Mismatches 68; Indels 89; Gaps 8;

```

DB 255 TR-FKTHASLGMYRF 270

RESULT 4

OPAC_NEIGO STANDARD: PRT: 236 AA.

AC P11296; 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA50 precursor (OPA30) (VO) (Fragment).
 GN OPA50.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RC STRAIN=MS11 / VO;
 RX MEDLINE=87002493; PubMed=3093085;
 RA Stern A., Brown M., Nickel P., Meyer T.F.;
 RT "Opacity genes in Neisseria gonorrhoeae: control of phase and
 RT antigenic variation.";
 RL Cell 47:61-71(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 RT epithelial cells.";
 RL EMO J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.

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CC EMBL; M14746; -; NOT_ANNOTATED_CDS.
 DR EMBL; Z18927; CA79360.1; -;
 DR PIR; A24429; KONHO.
 DR PIR; S28621; S28621.
 DR PIR; S36328; S36328.
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity.1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1
 FT CHAIN 2 >236 POTENTIAL.
 FT NON_TER 236 236 OPACITY PROTEIN OPA50.
 SQ SEQUENCE 236 AA; 26685 MW; 68DC237692183398 CRC64;

Query Match 27.0%; Score 234; DB 1; Length 236;
 Best Local Similarity 29.7%; Pred. No. 5e-14;
 Matches 71; Conservative 24; Mismatches 60; Indels 84; Gaps 9;

QY 17 ALAAGSGFYVQADAAHA-----KASSSLGSAKGF-----PRISAGY 54
 DB 1 ASEGGGPGPYQADLAYEYEHITHDYPKPTDPSKGKISTVSDYFRNIRTHSHPRVSAGY 60
 QY 55 RINDRFADVTRY-----KTKKASTD-----FKLYSIGAS 86
 DB 61 DFGGRRIADYARARKKMSDNKYSIKNMRYVHKHNSNKKLKTENQSGSFHVAVSLGLS 120
 QY 87 AIYDFDQSPVKPYLGARSLN--RASVD-----LGG----- 116

DB 121 AIYDFDQSPVKPYLGARSLN--RASVD-----LGG----- 116
 QY 117 -SDSFSQSTGLVAGVAVTPNVDDAGYRNYTKGKNTKYNVAGNSGLSAGYVRF 174
 DB 181 ESDSIR--VGLGVAGVAGFDITPKLTLDAGYRHHMGRLENT--FKTHASLGAVRYRF 236

RESULT 5

OPAB_NEIGO STANDARD: PRT: 234 AA.

AC 004874;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA51 precursor (Fragment).
 GN OPAB.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 RT epithelial cells.";
 RL EMO J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.

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CC EMBL; Z18928; CA79361.1; -;
 DR PIR; S28628; S28628.
 DR PIR; S36329; S36329.
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity.1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1
 FT CHAIN 2 >234 POTENTIAL.
 FT NON_TER 234 234 OPACITY PROTEIN OPA51.
 SQ SEQUENCE 234 AA; 26772 MW; 9FEF5B5DABA86CA CRC64;

Query Match 26.7%; Score 231.5; DB 1; Length 234;
 Best Local Similarity 29.9%; Pred. No. 8.2e-14;
 Matches 70; Conservative 23; Mismatches 62; Indels 79; Gaps 9;

QY 19 AEG-ASGFYVQADAAHA-----KASSSLGSAK-----GFSPRISAGR 55
 DB 2 SEGGGPGPYQADLAYEYEHITHDYPEGTGKDKISTVSDYFRNIRTHSHPRVSAGD 61
 QY 56 INDLRADVTRYK--NYKAPSTDFK-----LYSIGASATY 89
 DB 62 FGGWRRIADYARARKKNDKYSYDIKELKNKQNRKDKLTENQENGFHVAVSLGLSAY 121
 QY 90 DFTQSPVFPYLGARSLN--RASVD-----LGG-----SDSF 120
 DB 122 DFLNGKFRPYIGARVAAYGHVHSIDSTKTKTKFLTSYSGGLNPVTYTEENTQNAHHSN 181
 QY 121 SQSTSTGLVAGVAVTPNVDDAGYRNYTKGKNTKYNVAGNSGLSAGYVRF 174
 DB 182 SIKRVGLGVAGVAGFDITPKLTLDIGYRHHMGRLENT--FKTHASLGAVRYRF 234

RESULT 6
ID OPAJ_NEIGO STANDARD: PRT: 237 AA.
AC 004882;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA58 precursor (Fragment).
GN OPAJ.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
epithelial cells";
RT EMBO J. 12:641-650(1993).
RL
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
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CC -----
DR EMBL; Z18937; CAA79370.1; -.
DR PIR; S28624; S28624.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.
FT NON_TER 1 1
FT SIGNAL <1 1 POTENTIAL.
FT CHAIN 2 >237 OPACITY PROTEIN OPA58.
FT NON_TER 237 237
SQ SEQUENCE 237 AA; 26855 MW; B165033B2CDBA53 CRC64;
Query Match 26.7%; Score 231.5; DB 1; Length 237;
Best Local Similarity 30.0%; Pred. No. 8.3e-14;
Matches 70; Conservative 23; Mismatches 35; Indels 85; Gaps 9;
QY 24 GPYVQADAAHA-----KASSLSGSAKPS-----PRISAGYRINDLRF 61
DB 8 GPYVQADLAAYAYEHITHDYPQGTGPKDKISTVSDYFRNIRKTHSHPRVSVYDGFQGMRI 67
QY 62 AVDYTRKNT-----KAPSTDFK-----LYSIGSAIYDFTOS 93
DB 68 AADYARARKMNDNKYSVSIKELRNKRVNGNRKTRKTEONGTFHNAVSSLSGSAVYDFKL 127
QY 94 QSPKPYLGARLSLN--RASVD-----LGG-----SDSPSQTSTG 121
DB 128 NDKFKPYIGARVAVGAVRHSHIDSTKKTTEVTTILHGPCTTPPYPPKNTQDAHRESDSIR 187
QY 122 QSTGGLAVGSAVAVPNVDLAGRYNTYKNTVKNVSGELSGAYRVK 174
DB 188 R--VGLGAVAGVGDIDTPNLTLDAGRYHYHWRLENT-RFKTHEASLGVRVRF 237
RESULT 7
ID OPAJ_NEIGO STANDARD: PRT: 234 AA.
AC 004878;
DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA55 precursor (Fragment).
GN OPAJ.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
epithelial cells";
RT EMBO J. 12:641-650(1993).
RL
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z18933; CAA79366.1; -.
DR PIR; S28632; S28632.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.
FT NON_TER 1 1
FT SIGNAL <1 1 POTENTIAL.
FT CHAIN 2 >234 OPACITY PROTEIN OPA55.
FT NON_TER 234 234
SQ SEQUENCE 234 AA; 26881 MW; 8EBB30B3A774C766 CRC64;
Query Match 26.6%; Score 231; DB 1; Length 234;
Best Local Similarity 29.8%; Pred. No. 9.1e-14;
Matches 68; Conservative 22; Mismatches 60; Indels 78; Gaps 8;
QY 24 GPYVQADAAHA-----KASSLSGSAK-----GSPRISAGYRINDLRF 61
DB 8 GPYVQADLAAYAYEHITHDYPQGTGPKDKISTVSDYFRNIRKTHSHPRVSVYDGFQGMRI 67
QY 62 AVDYTRKNT-----KAPSTDFK-----LYSIGSAIYDFTOS 95
DB 68 AADYARARKMNDNKYSVSIKELRNKRVNGNRKTRKTEONGTFHNAVSSLSGSAVYDFKL 127
QY 96 PVKPYLGARLSLN--RASVD-----LGG-----SDSPSQTSTG 126
DB 128 KFKPYIGARVAVGAVRHSHIDSTKKTTRKLTSSYGLNPTVTEONTNAHQSISIRVG 187
QY 127 LGVAVGSAVAVPNVDLAGRYNTYKNTVKNVSGELSGAYRVK 174
DB 188 LGVAVGSAVAVPNVDLAGRYNTYKNTVKNVSGELSGAYRVK 174
RESULT 8
ID OPAJ_NEIGO STANDARD: PRT: 234 AA.
AC 004879;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA56 precursor (Fragment).
GN OPAJ.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;

```

RN SEQUENCE FROM N.A.
RC STRAIN-MS11 / F3;
RX MEDLINE-93178439; PubMed-8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells."
RL EMBO J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; 218934; CAI79367.1; -.
DR PIR; S28620; S28620.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.
FT SIGNAL 1 1
FT NON_TER 1 1
FT CHAIN 2 >234 POTENTIAL.
FT NON_TER 234 234 OPACITY PROTEIN OPA56.
SQ SEQUENCE 234 AA; 26868 MW; 5175C6606839EFFB CRC64;

Query Match
Best Local Similarity 26.6%; Score 231; DB 1; Length 234;
Matches 67; Conservative 23; Mismatches 60; Indels 78; Gaps 8;

QY 24 GFYVQADAAHA-----KASSSLGSAK-----GPSRISAGYRINDLRF 61
DB 8 GPYVQADLAAYEHITHDHPROTGTGKTKKIDISTVDFRNVRTHSHIPRVSVYDGGWRI 67
QY 62 ANDYTRYKNYKAP--STDFK-----LYSISASAIYDFDQS 95
DB 68 AADYATYRKWMDKYSVDIKELNNKONKRDKTENQENGTFHAYSLGSLAVYDFKLAND 127
QY 96 PVKPYIGARLSLN--RASVD-----LGG-----SDSFQSTSTG 126
DB 128 KRPYIIGARVAAGVHRHSIDSTKTKTKTLLTSSYGGILNPTVYTEMNTONAHHSIRRVG 187
QY 127 LCVLAGVSYAVTPNVDLDAGYRYNTIGKYNVKNRSGELSGAVRYKF 174
DB 188 LCVIAGVGFDITPKLTDGYRYHWMGRLENTR-FKTHASLSGVYRFR 234

RESULT 9
OP67_NEIGO STANDARD; PRT; 233 AA.
AC 05034;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA67 precursor (Fragment).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Vp1;
RX MEDLINE-93178439; PubMed-8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells."

```

```

RL EMBO J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; 218942; CAI79375.1; -.
DR PIR; S28625; S28625.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.
FT SIGNAL 1 1
FT NON_TER 1 1
FT CHAIN 2 >233 POTENTIAL.
FT NON_TER 233 233 OPACITY PROTEIN OPA67.
SQ SEQUENCE 233 AA; 26039 MW; 6C13A46AB163C67F CRC64;

Query Match
Best Local Similarity 26.5%; Score 230; DB 1; Length 233;
Matches 65; Conservative 29; Mismatches 61; Indels 78; Gaps 7;

QY 19 AEG-ASGYVQADAAHA-----KASSSLGSAKG-----SPRISAGY 54
DB 2 SEGNGRGPYVQADLAAYERITHDYPETAQKCKGTISTVSDYRNIRTHSVHPRVSVG 61
QY 55 RINDRFAPVDYTRYKNY-----KAPSDFKLYSTIGSAIYDFD 92
DB 62 DFGKRIADYARIRKMNKSYISIKLONQYKKTENQENGTFHASSLSGSAVYDFK 121
QY 93 TQSPYKPYIGARLSLN--RASVDL-----GGSDFS 121
DB 122 LNDKFKPYIGARVAAGVHRHSIDSTKTKTGTGTTAGARGAAPVSSPYKNTQADHQSNS 181
QY 122 QTSVGLVLAGVSYAVTPNVDLDAGYRYNTIGKYNVKNRSGELSGAVRYKF 174
DB 182 IRRVGLVLAGVGFDITPKLTDGYRYHWMGRLENTR-FKTHASLSGVYRFR 233

RESULT 10
OP28_NEIGO STANDARD; PRT; 234 AA.
AC P11297;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Opacity protein V28 precursor (Fragment).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-87002493; PubMed-3093085;
RA Stern A., Brown M., Nickel P., Meyer T.F.;
RT "opacity genes in Neisseria gonorrhoeae: control of phase and
RT antigenic variation."
RL Cell 47:61-71(1986).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
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Best Local Similarity 28.9%; Pred. No. 3.2e-13;
Matches 67; Conservative 25; Mismatches 58; Indels 82; Gaps 8;

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QY 24 GFYVQADAAHA-----KASSSLGSAKF-----SPRISAGYRINDLR 61
D 8 GPYVQADLAAYEHITHDYPKPTDPSGKRLSTVSDYFRNTRTSHPRVSGVDEGKWL 67
QY 62 AVDYTRK--NYKAPSDER-----LYSIGASAIYDFDT 93
D 68 AADYTRKRNKNDKSYSTINKLQRTSNGNRDRKTENQENGSHAVSSIGLSAVYDFKL 127
QY 94 QSPVKKPYLGARLSLN--RASVD-----LGSD-----SPSQ 122
D 128 NDKFKPYIGARVAYGVHRHSIDSTKKTETETITAGARGTDPYSSPYKNTQDAHQESNSI 187
QY 123 TSTGLVAGVSAVTPNDLDAGRYNNGKYNVKNVRSGLSAGVRYKF 174
D 188 RRVGLVAGVGPDIPTNLLDAGRYHMGWRLNTR-FKTHASLGVRYRF 238

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RESULT 13

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ID OPAH_NEIGO STANDARD; PRT; 238 AA.
AC 004884;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Opacity protein OPA60 precursor (Fragment).
GN OPAH.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells."
RL EMO J. 12:641-650(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / V18;
RX MEDLINE=92114767; PubMed=1815562;
RA Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnis F.,
RA Stern A., Kupsch E.-M., Meyer T.F., Swanson J.;
RT "The opacity proteins of Neisseria gonorrhoeae strain MS11 are
RT encoded by a family of 11 complete genes."
RL Mol. Microbiol. 5:1889-1901(1991).
RN [3]
RP ERRATUM.
RX MEDLINE=92261323; PubMed=1584024;
RA Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnis F.,
RA Stern S., Kupsch E.-M., Meyer T.F., Swanson J.;
RL Mol. Microbiol. 6:1073-1076(1992).

```

-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
VARIATION.

-1- SUBCELLULAR LOCATION: Outer membrane.

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DR EMBL; Z18939; CAA79372.1; -;
DR EMBL; X60711; CAA43121.1; -;
DR PIR; S28631; S28631.
DR InterPro; IPR003394; Opacity.

DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.

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FT SIGNAL 1
FT CHAIN 1
FT VARIANT 2 >238 POTENTIAL.
FT VARIANT 234 4 OPACITY PROTEIN OPA60.
FT NON_TER 234 234 SED -> MKK (IN MS11 / V18).
SO SEQUENCE 238 AA; 27073 MW; 883A3560C2DF1B9F CRC64;

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Query Match 25.9%; Score 225; DB 1; Length 238;
Best Local Similarity 28.0%; Pred. No. 3.2e-13;

Matches 67; Conservative 24; Mismatches 66; Indels 82; Gaps 6;

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QY 17 ALAEGASGFYVQADAAHA-----KASSSLG-----AKGFSRISAGY 54
D 1 ASEDGGRPYVQADLAAYEHITHDYPEPTAPNKNKISTVSDYFRNTRTSHPRVSGV 60
QY 55 RINDLRFAVDYTRKKNY-----KASTDFKLYSIGAS 86
D 61 DFGWRRIADYARRKNNKNNKYSNIENVRIKENGIRIDRKTENQENGTFHAVSSIGLS 120
QY 87 AYPDPTQSPKPYIGARLSLN--RASVD-----LG 115
D 121 AYPQINDKRPYIGARVAYGVHRHSIDSTKKTETETVPSNAPNGAVTYTNDPKTN 180
QY 116 GSDSPQSTGSLVAGVSAVTPNDLDAGRYNNGKYNVKNVRSGLSAGVRYKF 174
D 181 DYGSNIRVGLVAGVGPDIPTNLLDAGRYHMGWRLNTR-FKTHASLGVRYRF 238

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RESULT 14

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ID OPAD_NEIGO STANDARD; PRT; 243 AA.
AC 004883;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA59 precursor (Fragment).
GN OPAD.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells."
RL EMO J. 12:641-650(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / V18;
RX MEDLINE=92114767; PubMed=1815562;
RA Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnis F.,
RA Stern A., Kupsch E.-M., Meyer T.F., Swanson J.;
RT "The opacity proteins of Neisseria gonorrhoeae strain MS11 are
RT encoded by a family of 11 complete genes."
RL Mol. Microbiol. 5:1889-1901(1991).
RN [3]
RP ERRATUM.
RX MEDLINE=92261323; PubMed=1584024;
RA Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnis F.,
RA Stern S., Kupsch E.-M., Meyer T.F., Swanson J.;
RL Mol. Microbiol. 6:1073-1076(1992).

```

-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
VARIATION.

-1- SUBCELLULAR LOCATION: Outer membrane.

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DR EMBL; Z18938; CAA79371.1; -;
DR PIR; S28629; S28629.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.
FT NON_TER 1
FT SIGNAL 1
FT CHAIN 2 >243 POTENTIAL.
FT CHAIN 2 >243 OPACITY PROTEIN OPA59.

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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:56:04 ; Search time 19.9713 Seconds
(without alignments)
1507.218 Million cell updates/sec

Title: US-09-684-883-6

Perfect score: 1 MKKALATLRLALPAALAE.....VNTVKNVSGELSGVRYKVF 174

Sequence: BL0SUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_TREMBL_19:*
2: SP_Bacteria:*
3: SP_Fungi:*
4: SP_Human:*
5: SP_Invertebrate:*
6: SP_Mammal:*
7: SP_Mhc:*
8: SP_Organelle:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Rodent:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*
15: SP_Virus:*
16: SP_Bacteriophage:*
17: SP_Archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	174	16	P95372
2	866	99.8	174	2	Q9RP16
3	862	99.3	174	2	Q9R2R1
4	860	99.1	174	2	Q9RP18
5	858	98.8	174	16	Q9RP17
6	854	98.4	174	2	P96943
7	838.5	96.6	175	2	P95371
8	834	96.1	174	2	P95343
9	246	28.3	256	2	051124
10	243.5	28.1	186	16	Q9CRL9
11	243.5	28.1	241	2	Q9AEB0
12	243	28.0	234	2	Q9R719
13	243	28.0	234	2	007280
14	242	27.9	234	2	Q9R718
15	240.5	27.7	232	2	Q9K4F9
16	240	27.6	237	2	031176

17	239.5	27.6	230	2	Q9R9A7	Q9R9A7 neisseria m
18	239	27.5	241	2	Q9K4T4	Q9K4T4 neisseria l
19	239	27.5	256	2	051126	051126 neisseria m
20	239	27.5	259	2	051125	051125 neisseria m
21	238.5	27.5	232	2	Q9R3P5	Q9R3P5 neisseria m
22	238	27.4	270	2	Q9R0V4	Q9R0V4 neisseria m
23	237.5	27.4	257	2	Q50929	Q50929 neisseria m
24	237	27.3	234	2	007287	007287 neisseria f
25	236.5	27.2	241	2	007274	007274 neisseria m
26	236	27.2	262	2	033388	033388 neisseria m
27	235.5	27.1	232	2	Q9K4T3	Q9K4T3 neisseria s
28	235.5	27.1	241	2	007912	007912 neisseria s
29	235	27.1	283	2	Q50943	Q50943 neisseria m
30	233	26.8	240	2	007925	007925 neisseria m
31	233	26.8	272	2	051013	051013 neisseria m
32	232.5	26.8	253	2	051303	051303 neisseria s
33	232	26.7	233	2	Q9K4T5	Q9K4T5 neisseria l
34	232	26.7	235	2	030753	030753 neisseria l
35	231.5	26.7	232	2	Q9R9A9	Q9R9A9 neisseria m
36	231.5	26.7	232	2	Q9R9A8	Q9R9A8 neisseria m
37	231	26.6	237	2	Q9K4T6	Q9K4T6 neisseria l
38	230.5	26.6	241	2	007273	007273 neisseria m
39	230	26.5	235	2	030752	030752 neisseria m
40	228.5	26.3	232	2	Q9K4T7	Q9K4T7 neisseria l
41	227	26.2	242	2	Q9K4T8	Q9K4T8 neisseria l
42	226.5	26.1	238	2	031172	031172 neisseria m
43	226.5	26.1	243	2	007278	007278 neisseria m
44	226	26.0	237	2	031175	031175 neisseria m
45	226	26.0	260	2	033389	033389 neisseria m

ALIGNMENTS

RESULT 1
P95372 PRELIMINARY; PRT; 174 AA.
AC P95372;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE OUTER MEMBRANE PROTEIN PRECURSOR.
GN NSPA OR NMA0862.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup A).
OC Bacteria: Proteobacteria: beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487, 65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=24063;
RA Martin D., Cadieux N., Hamel J., Rioux C., Brodeur B.R.;
RN Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajadream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491."
RT Nature 404:502-506(2000).
DR EMBL: U52068; AAB41580.1; -
DR EMBL: AL162754; CAB84143.1; -
DR InterPro: IPR003394; Opacity; 1.
DR Pfam: PF02462; Opacity; 1.
KM Signal: Complete proteome.
FT SIGNAL. 1 19 POTENTIAL.
SQ SEQUENCE 174 AA; 18355 MW; EBA4A1ADAFA6F009 CRC64;

Query Match 100.0%; Score 866; DB 16; Length 174;
 Best Local Similarity 100.0%; Pred. No. 1.2e-64;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKKALATLIALPAALAEAGSGFYVOADAHAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAALAEAGSGFYVOADAHAHAKASSLSGAKGSPRISAGYRINDLR 60

OY 61 FAVDYTRYKKNYKAPSTDFEKLKYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120
 DB 61 FAVDYTRYKKNYKAPSTDFEKLKYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120

OY 121 SQTSTGLGVLGAGSYAVTPNVDLDAGYRNYIGKVNIVKVRSGELSGAGYRVKF 174
 DB 121 SQTSTGLGVLGAGSYAVTPNVDLDAGYRNYIGKVNIVKVRSGELSGAGYRVKF 174

RESULT 2

O9RP16 PRELIMINARY; PRT; 174 AA.

ID O9RP16
 AC O9RP16;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
 DE SURFACE PROTEIN A.
 GN NSPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NG3/88;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 DR EMBL; AF175681; AAD53284.1; -.
 DR InterPro; IPR003394; Opacity. 1.
 DR Pfam; PF02462; Opacity. 1.
 SO SEQUENCE 174 AA; 18355 MW; ECF6F38B9286800E CRC64;

Query Match 99.8%; Score 866; DB 2; Length 174;
 Best Local Similarity 99.4%; Pred. No. 1.8e-64;
 Matches 173; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKKALATLIALPAALAEAGSGFYVOADAHAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAALAEAGSGFYVOADAHAHAKASSLSGAKGSPRISAGYRINDLR 60

OY 61 FAVDYTRYKKNYKAPSTDFEKLKYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120
 DB 61 FAVDYTRYKKNYKAPSTDFEKLKYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120

OY 121 SQTSTGLGVLGAGSYAVTPNVDLDAGYRNYIGKVNIVKVRSGELSGAGYRVKF 174
 DB 121 SQTSTGLGVLGAGSYAVTPNVDLDAGYRNYIGKVNIVKVRSGELSGAGYRVKF 174

RESULT 3

O9R2R1 PRELIMINARY; PRT; 174 AA.

ID O9R2R1
 AC O9R2R1;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
 DE SURFACE PROTEIN A.
 GN NSPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M136, AND B232;

RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 DR EMBL; AF175679; AAD53282.1; -.
 DR EMBL; AF175677; AAD53280.1; -.
 DR InterPro; IPR003394; Opacity. 1.
 DR Pfam; PF02462; Opacity. 1.
 SO SEQUENCE 174 AA; 18385 MW; ECF6F39A9286910E CRC64;

Query Match 99.3%; Score 862; DB 2; Length 174;
 Best Local Similarity 98.9%; Pred. No. 3.8e-64;
 Matches 172; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKKALATLIALPAALAEAGSGFYVOADAHAHAKASSLSGAGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAALAEAGSGFYVOADAHAHAKASSLSGAGSPRISAGYRINDLR 60

OY 61 FAVDYTRYKKNYKAPSTDFEKLKYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120
 DB 61 FAVDYTRYKKNYKAPSTDFEKLKYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120

OY 121 SQTSTGLGVLGAGSYAVTPNVDLDAGYRNYIGKVNIVKVRSGELSGAGYRVKF 174
 DB 121 SQTSTGLGVLGAGSYAVTPNVDLDAGYRNYIGKVNIVKVRSGELSGAGYRVKF 174

RESULT 4

O9RP18 PRELIMINARY; PRT; 174 AA.

ID O9RP18
 AC O9RP18;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
 DE SURFACE PROTEIN A.
 GN NSPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8047;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 DR EMBL; AF175676; AAD53279.1; -.
 DR InterPro; IPR003394; Opacity. 1.
 DR Pfam; PF02462; Opacity. 1.
 SO SEQUENCE 174 AA; 18357 MW; 0205A1DA1B7F005 CRC64;

Query Match 99.1%; Score 860; DB 2; Length 174;
 Best Local Similarity 98.9%; Pred. No. 5.5e-64;
 Matches 172; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKKALATLIALPAALAEAGSGFYVOADAHAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAALAEAGSGFYVOADAHAHAKASSLSGAKGSPRISAGYRINDLR 60

OY 61 FAVDYTRYKKNYKAPSTDFEKLKYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120
 DB 61 FAVDYTRYKKNYKAPSTDFEKLKYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120

OY 121 SQTSTGLGVLGAGSYAVTPNVDLDAGYRNYIGKVNIVKVRSGELSGAGYRVKF 174
 DB 121 SQTSTGLGVLGAGSYAVTPNVDLDAGYRNYIGKVNIVKVRSGELSGAGYRVKF 174

RESULT 5

O9RP17 PRELIMINARY; PRT; 174 AA.

ID O9RP17
 AC O9RP17;
 DT 01-MAY-2000 (TREMblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DE SURFACE PROTEIN A (OUTER MEMBRANE PROTEIN NSGA).
 GN NSPA OR NMB0663.
 OS Neisseria meningitidis, and
 OC Neisseria meningitidis (serogroup B).
 RX Bacteria: Proteobacteria; beta subdivision: Neisseriaceae; Neisseria.
 NX NCBI_TaxID=487, 491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CU385;
 RT Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC58 / SEROGROUP B;
 RX MEDLINE=20175755; PubMed=10710307;
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gillin M.T., Deboy R., Peterson J.D., Hickey E.K.,
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Ciecko A., Parksey D.S., Blair E., Cifton H., Clark E.B.,
 RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
 RA Gill J., Scarlato V., Maignani V., Pizzi M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58.";
 RL Science 287:1809-1815 (2000).
 DR EMBL: AF175678; AAD53281.1;
 DR EMBL: AE002420; AAF41081.1;
 DR TIGR: NMB0663;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Complete proteome.
 SQ SEQUENCE 174 AA; 18397 MW; E8B02767DDC6E109 CRC64;

Query Match 98.8%; Score 858; DB 16; Length 174;
 Best Local Similarity 98.9%; Pred. No. 8.1e-64;
 Matches 172; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGGSDSF 120
 QY 121 SQTSTGLVLAGSVYAVTPNVLDAGYRNYTGKNTYKVRSGELSGYRKF 174
 DB 121 SQTSTGLVLAGSVYAVTPNVLDAGYRNYTGKNTYKVRSGELSGYRKF 174

RESULT 6
 ID P96943 PRELIMINARY; PRT; 174 AA.
 AC P96943;
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE OUTER MEMBRANE PROTEIN PRECURSOR.
 GN NSPA.
 OS Neisseria meningitidis.
 OC Bacteria: Proteobacteria; beta subdivision: Neisseriaceae; Neisseria.
 NX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=608B;
 RX MEDLINE=97149429; PubMed=8996237;
 RA Martin D., Cadieux N., Hamel J., Brodeur B.R.;
 RT "Costimulation of T cell activation by integrin-associated protein

RT (CD47) is an adhesion-dependent, CD28-independent signaling pathway.";
 RL J. Exp. Med. 185:1-11(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NGP165, M986, AND NG6/88;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 DR EMBL: AF175683; AAD53286.1;
 DR EMBL: AF175680; AAD53283.1;
 DR EMBL: AF175682; AAD53285.1;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Signal.
 FT SIGNAL 1
 SQ SEQUENCE 174 AA; 18425 MW; E8B02767DDC6E19 CRC64;

Query Match 98.4%; Score 854; DB 2; Length 174;
 Best Local Similarity 98.3%; Pred. No. 1.7e-63;
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGGSDSF 120
 QY 121 SQTSTGLVLAGSVYAVTPNVLDAGYRNYTGKNTYKVRSGELSGYRKF 174
 DB 121 SQTSTGLVLAGSVYAVTPNVLDAGYRNYTGKNTYKVRSGELSGYRKF 174

RESULT 7
 ID P95371 PRELIMINARY; PRT; 175 AA.
 AC P95371;
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE OUTER MEMBRANE PROTEIN PRECURSOR.
 OS Neisseria meningitidis.
 OC Bacteria: Proteobacteria; beta subdivision: Neisseriaceae; Neisseria.
 NX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MCH 88;
 RX MEDLINE=99386904; PubMed=10456958;
 RA Cadieux N., Plante M., Rioux C.R., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
 RT "Bactericidal and cross-protective activities of a monoclonal antibody
 directed against Neisseria meningitidis Nspa outer membrane protein.";
 RL Infect. Immun. 67:4955-4959(1999).
 DR EMBL: U52067; AAB41579.1;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Signal.
 FT SIGNAL 1
 SQ SEQUENCE 175 AA; 18572 MW; D1EABF2F5C22FEA CRC64;

Query Match 96.6%; Score 838.5; DB 2; Length 175;
 Best Local Similarity 97.1%; Pred. No. 3.4e-62;
 Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGGSDSF 119
 DB 61 FAVDYTRYKNYKAPSTDFLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGGSDSF 120

QY 120 FSGTSTGLGVLGAGSYAVTPNVDLAGRYNYIGKVTYKVRSGELSGAGYRVKF 174
 DB 121 FSGTSTGLGVLGAGSYAVTPNVDLAGRYNYIGKVTYKVRSGELSGAGYRVKF 175

RESULT 8
 P95343 PRELIMINARY; PRT; 174 AA.
 AC P95343;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE OUTER MEMBRANE PROTEIN PRECURSOR.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B2;
 RX MEDLINE=99270944; PubMed=10338491;
 RA Plante M., Cadieux N., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
 RT Antigenic and molecular conservation of the gonococcal Nspa
 RT protein.";
 RL Infect. Immun. 67:2855-2861(1999).
 DR EMBL: U52069; AAB41581.1; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW SIGNAL.
 FT SIGNAL.
 SQ SEQUENCE 1 19 POTENTIAL.
 18337 MW; 18558EC8A040841A CRC64;

Query Match 96.1%; Score 834; DB 2; Length 174;
 Best Local Similarity 95.4%; Pred. No. 8e-62; Mismatches 6; Indels 0; Gaps 0;
 Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKKALATLALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60

QY 61 FAVDYTRYKRYKAPSTDFKITYSGASAYDFQSPVKPYPLGARLSLNKASVDLGSDSE 120
 DB 61 FAVDYTRYKRYKAPSTDFKITYSGASAYDFQSPVKPYPLGARLSLNKASVDLGSDSE 120

QY 121 SGTSTGLGVLGAGSYAVTPNVDLAGRYNYIGKVTYKVRSGELSGAGYRVKF 174
 DB 121 SGTSTGLGVLGAGSYAVTPNVDLAGRYNYIGKVTYKVRSGELSGAGYRVKF 174

RESULT 9
 O51124 PRELIMINARY; PRT; 256 AA.
 ID O51124;
 AC O51124;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE OPACITY OUTER MEMBRANE PROTEIN (FRAGMENT).
 OX OPA.
 GN Neisseria meningitidis.
 OS Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OC NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=24197;
 RX MEDLINE=98129089; PubMed=9467908;
 RA Hobbs M.M., Majorry B., Prasad P., Morelli G., Kusecek B.,
 RA Heckels J.E., Cannon J.G., Achtman M.;
 RT "Recombinational reassortment among opa genes from FT-37 complex
 RT Neisseria meningitidis isolates of diverse geographical origins.";
 RL Microbiology 144:157-166(1998).
 DR EMBL: U37255; AAC46101.1; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.

FT NON TER 1 1
 SQ SEQUENCE 256 AA; 28335 MW; 9DA1C6079C6DD13F CRC64;
 Query Match 28.3%; Score 246; DB 2; Length 256;
 Best Local Similarity 28.7%; Pred. No. 8.3e-13;
 Matches 70; Conservative 31; Mismatches 65; Indels 78; Gaps 7;

QY 8 LIALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 170
 DB 14 LFSSAQAQASDSDSCHGPRYVQADLAVERITHDYPRAQANNSTSVSDYERNIRAHSH 73

QY 48 PRISAGYRINDLRPAVDYTRYK-----NYAPSTDR-----LIS 82
 DB 74 PRVSQYDFGGMRIADYASRYKWKESNSPKKVTEDIANRYETKEHQNGSFFHAASS 133

QY 83 IGASAYDFQSPVKPYPLGARLSLNK-----ASVDLG----- 116
 DB 134 LGLSAYDFKINDKFKPYPLGARVAYGKQHVSVETKTTVSKPATSPQGGPIIQND 193

QY 117 -----SDPSQSTGLGVLGAGSYAVTPNVDLAGRYNYIGKVTYKVRSGELSGAGY 170
 DB 194 PSKPPYHSHSSLSGLGVLGAGVFDTLPKLTDTGYRHNWGRLENT-R-FKTHEVSLGW 252

QY 171 RVKF 174
 DB 253 RYRF 256

RESULT 10
 O9CM19 PRELIMINARY; PRT; 186 AA.
 ID O9CM19;
 AC O9CM19;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE OPA.
 GN PASTEURILLA MULTOCIDA.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PM70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida pm70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 DR EMBL: AF006143; AAK03109.1; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Complete proteome.
 SQ SEQUENCE 186 AA; 20512 MW; 1B17F0A4AFC0157 CRC64;

Query Match 28.1%; Score 243.5; DB 16; Length 186;
 Best Local Similarity 32.3%; Pred. No. 9e-13;
 Matches 61; Conservative 31; Mismatches 78; Indels 19; Gaps 5;

QY 1 MKKALATLALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRIN 57
 DB 2 MKK-----SILVLAIGALCSLTASANYVQDGLCAVKTKFSSSEMMKNTIYVNVSGYDLG 58

QY 58 DIRPAVDTRYKRYKAP-----TDFKLYSGASAYDFQSPVKPYPLGARLSLN 108
 DB 59 AARLADLTHYKFGSTSFEGVNOKEHVSTKYIGLSAFYDFTNSVLAQFYVRLASN 118

QY 109 RASVDLGSDSE-----SGTSTGLGVLGAGSYAVTPNVDLAGRYNYIGKVTYKVRSGE 165
 DB 119 IDIENKGSNFRSEKTKLGYGTAGQYGLMTNLFVNGGIEYVRLGRFSDT-SVNGYG 177

QY 166 LSAQYRVKF 174
 DB 178 AKVGLKRYDF 186

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RP SEQUENCE FROM N.A.
RC STRAIN-3926:
RA Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Linz B.,
RA Popovic T., Schuurman I.G.A., Adegola R.A., Zuth K., Gagneux S.,
RA Papanov A.E., Rhou J.Y., Gaugant D.A., Nicolas P., Achtman M.,
RT "Fit genotypes and escape variants of subgroup III Neisseria
RT meningitidis during three pandemics of epidemic meningitidis."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBU databases.
DR EMBL: AF001194; AAC32715.1; -
DR EMBL: AJ292235; CAC36358.1; -
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity: 1.
DR NON_TER 1
SQ SEQUENCE 234 AA; 26161 MW; F97142P463136EC1 CRC64;

Query Match 28.0%; Score 243; DB 2; Length 234;
Best Local Similarity 29.3%; Pred. No. 1.3e-12;
Matches 68; Conservative 30; Mismatches 60; Indels 74; Gaps

OY 16 AALAEGA-SGFYVQADAAH-----AKKSSSLGS-----AKGSPRISAGY 54
DB 4 AASEDGSSPFYVQADLAIAERITHTDYPQATGANNSTVSDYFNRINRAHS:HPRVSVGY 63
OY 55 RINDLRPAVDYTRYK-----NYKAPSTDEK-----LYSIGASAI 88
DB 64 DFGDMRIADVAASYRKMKESNYSKVTEFKHQGNKQOEKTEHQNGSPHATSIGLSAI 123
OY 89 YDEPTQSPVRYLYGARLSLNR-----ASVDLGG-----SDSFSQ 122
DB 124 YDFRLNDKFPYIGVRAVGAHVHQAHSVESKTTVTWTTNGSGPVPQGPPTKPAVHESHSI 183
OY 123 TSTSLGLAIVSYAVTPNVVDLAGYRYNIGKVVYKVNRSGLSAGRVAF 174
DB 184 SSVGLGVIAAGVGDITPRLTLDIGYKTHMWRGLENTF-KTHVEYSLGRHF 234

RESULT 13
O07280 PRELIMINARY; PRT: 234 AA.
AC 007280:
DT 01-JUL-1997 (TEMBLrel. 04, Created)
DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE OPACITY PROTEIN (FRAGMENT).
GN OPA.
OS Neisseria meningitidis.
OC Bacteria, Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxId=487;
RN SEQUENCE FROM N.A.
RP 11
RC STRAIN-23524;
RX MEDLINE=98010345; PubMed=9350862;
RX Morelli G., Malorny B., Muller K., Seiler A., Wang J.F., del Valle J.,
RA Achtman M.,
RT "Clonal descent and microevolution of Neisseria meningitidis during 30
RT years of epidemic spread."
RT MOL. Microbiol. 25:1047-1064(1997).
DR EMBL: AF001195; AAC32716.1; -
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity: 1.
DR NON_TER 1
SQ SEQUENCE 234 AA; 26134 MW; 005AD356E93BC50 CRC64;

Query Match 28.0%; Score 243; DB 2; Length 234;
Best Local Similarity 29.3%; Pred. No. 1.3e-12;
Matches 68; Conservative 30; Mismatches 60; Indels 74; Gaps

OY 16 AALAEGA-SGFYVQADAAH-----AKKSSSLGS-----AKGSPRISAGY 54
DB 4 AASEDGSSPFYVQADLAIAERITHTDYPQATGANNSTVSDYFNRINRAHS:HPRVSVGY 63
OY 55 RINDLRPAVDYTRYK-----NYKAPSTDEK-----LYSIGASAI 88
DB 64 DFGDMRIADVAASYRKMKESNYSKVTEFKHQGNKQOEKTEHQNGSPHATSIGLSAI 123
OY 89 YDEPTQSPVRYLYGARLSLNR-----ASVDLGG-----SDSFSQ 122
DB 124 YDFRLNDKFPYIGVRAVGAHVHQAHSVESKTTVTWTTNGSGPVPQGPPTKPAVHESHSI 183
OY 123 TSTSLGLAIVSYAVTPNVVDLAGYRYNIGKVVYKVNRSGLSAGRVAF 174
DB 184 SSVGLGVIAAGVGDITPRLTLDIGYKTHMWRGLENTF-KTHVEYSLGRHF 234

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DB 64 DFGDMRIADIVSYRKWKESNTSKVTEPKHONGKOEDEKTEHOGNGSFHATSLGLSAI 123
QY 89 YDFDTQSPVKPYLGARLSLNR-----ASVDLGG-----SDSFSQ 122
DB 124 YDFKLSDKRKPPIGVAVAGVHKQHVSVESKTTVTNNNGPVPQGPTRKPAYHESH1 183
QY 123 TSTGLGVLAGVSYAVTPNVDLAGRYNIGKVNIVKNNRSGELSGAVRYKF 174
DB 184 SSVGLGVLAGVGDITPKLLDTGYRYHNMGRLENTR-FKTHEVSLGMRHYF 234

RESULT 14
ID 09R718 PRELIMINARY; PRT: 234 AA.
AC 09R718;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE OPACITY PROTEIN (FRAGMENT).
GN OPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN 11
RP SEQUENCE FROM N.A.
RC MEDLINE=98010345; PubMed=9350862;
RA Morelli G., Malorny B., Muller K., Seiler A., Wang J.F., del Valle J.,
RT "Clonal descent and microevolution of Neisseria meningitidis during 30
RT years of epidemic spread."
RL Mol. Microbiol. 25:1047-1064(1997).
DR EMBL: AF001196; AAC32717.1;
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity; 1.
FT NON_TER 1
SQ SEQUENCE 234 AA; 26191 MW; F01D3B9163066171 CRC64;

Query Match 27.7%; Score 240.5; DB 2; Length 232;
Best Local Similarity 30.9%; Pred. No. 2.1e-12;
Matches 71; Conservative 29; Mismatches 65; Indels 65; Gaps 8;

QY 16 AALAEGA-SGFYVOADAHA--KASSSLGSAK-----ESPRIAGY 54
DB 4 AASDGRSPRYVQADLAVERTHDYPOATGANNSTVSDYFRNIRTHSHIPRYSVG 63
QY 55 RINDLRAVDYTRYK-----NYKAPSTDEK-----LYSIGASAI 88
DB 64 DFGDMRIADIVSYRKWKESNTSKVTEPKHONGKOEDEKTEHOGNGSFHATSLGLSAI 123
QY 89 YDFDTQSPVKPYLGARLSLNR-----ASVDLGG-----SDSFSQ 122
DB 124 YDFKLSDKRKPPIGVAVAGVHKQHVSVESKTTVTNNNGPVPQGPTRKPAYHESH1 183
QY 123 TSTGLGVLAGVSYAVTPNVDLAGRYNIGKVNIVKNNRSGELSGAVRYKF 174
DB 184 SSVGLGVLAGVGDITPKLLDTGYRYHNMGRLENTR-FKTHEVSLGMRHYF 234

RESULT 15
ID 09K4T9 PRELIMINARY; PRT: 232 AA.
AC 09K4T9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE OPA PROTEIN PRECURSOR (FRAGMENT).
GN OPA.
OS Neisseria lactamica.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=486;
RN 11
RP SEQUENCE FROM N.A.

```

```

RC SRRAIN-G501;
RA Toleman M.A., Aho E., Virji M.;
RT "Antigenic relatedness of commensal and pathogenic neisserial adhesins
RT genetic and functional analyses of commensal Opa proteins."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ288888; CAB93949.1;
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity; 1.
KW Signal.
FT NON_TER 1
FT SIGNAL <1 13 POTENTIAL.
FT CHAIN 14 >232 OPA A PROTEIN.
FT NON_TER 232
SQ SEQUENCE 232 AA; 26094 MW; 36FAAE60A3C014AF CRC64;

Query Match 27.7%; Score 240.5; DB 2; Length 232;
Best Local Similarity 30.9%; Pred. No. 2.1e-12;
Matches 71; Conservative 29; Mismatches 65; Indels 65; Gaps 8;

QY 6 AALAEGA-SGFYVOADAHA--KASSSLGSAK-----ESPRIAGY 54
DB 3 SLEFSSAVQANEDNGRGPVQADLYAVAEHTHDYPGNNAKLFDDYRDVKTSTHPR 62
QY 51 SAGYRINDLRPAVDYTRYK-----APSTD--FKLVS-IG 84
DB 63 SVGYDFGNMRTALDYARVYKWKHGKHLRTEQNKSVQNGTSVKLLADHTDGTFRKAE 122
QY 85 ASATYDFDTQSPVKPYLGARLSLNR-----ASVDLGG-----SDSFS 121
DB 123 ISATYDFDTGTRFRPYGAVRGLGKIRKSTALEKAEIIGNITSGGLKDAHPRIHSH 162
QY 123 TSTGLGVLAGVSYAVTPNVDLAGRYNIGKVNIVKNNRSGELSGAVRYKF 174
DB 183 IRRVGFAGVAGVGDITPKLLDTGYRYHNMGRLENTR-FKTHEVSLGMR 231

Search completed: October 28, 2002, 16:02:39
Job time : 20.9713 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:55:03 ; Search time 24.7145 Seconds
(without alignments)
782.004 Million cell updates/sec

Title: US-09-684-883-8
Perfect score: 870
Sequence: 1 MKKALALALALPAAALAE.....VNFVKNVBSGELSAGVRVK 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A.Geneseq.032802.*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	870	100.0	174	17	AAW04894
2	834	95.9	174	17	AAW04893
3	825	94.8	174	17	AAW04891
4	813.5	93.5	175	17	AAW04892
5	747	85.9	155	22	AA19895
6	133	15.3	25	17	AAW04912
7	125	14.4	170	16	AAW04911
8	106	12.2	353	22	AAW04911
9	101	11.6	359	16	AAW04911
10	96	11.0	369	21	AAW04911
11	96	11.0	369	21	AAW04911

12	95.5	11.0	212	22	AAW04894
13	95	10.9	257	22	AAW04893
14	95	10.9	369	20	AAW04891
15	94.5	10.9	797	20	AAW04892
16	92	10.6	364	21	AAW04893
17	92	10.6	364	21	AAW04894
18	92	10.6	364	21	AAW04895
19	90	10.3	500	22	AAW04896
20	87.5	10.1	573	19	AAW04897
21	87	10.0	16	17	AAW04898
22	86.5	9.9	215	21	AAW04899
23	86.5	9.9	215	21	AAW04900
24	86	9.9	568	17	AAW04901
25	83.5	9.6	339	21	AAW04902
26	83.5	9.6	534	21	AAW04903
27	83	9.5	610	19	AAW04904
28	83	9.5	624	19	AAW04905
29	83	9.5	889	19	AAW04906
30	81.5	9.4	162	17	AAW04907
31	81.5	9.4	708	19	AAW04908
32	81.5	9.4	708	21	AAW04909
33	81	9.3	279	17	AAW04910
34	81	9.3	350	9	AAW04911
35	81	9.3	350	22	AAW04912
36	80	9.2	15	17	AAW04913
37	80	9.2	259	21	AAW04914
38	80	9.2	260	20	AAW04915
39	80	9.2	260	20	AAW04916
40	80	9.2	270	19	AAW04917
41	80	9.2	270	19	AAW04918
42	80	9.2	270	21	AAW04919
43	80	9.2	270	21	AAW04920
44	80	9.2	273	18	AAW04921
45	80	9.2	273	18	AAW04922

ALIGNMENTS

RESULT 1	AAW04894	standard; Protein: 174 AA.
ID	AAW04894	
AC	AAW04894	
XX	22-DEC-1996	(first entry)
DT		
XX		
DE	Proteinase K resistant N. meningitidis 22 kd surface protein.	
XX		
KW	Proteinase K resistant; Neisseria meningitidis;	
KW	Neisseria gonorrhoeae; antibody; detection; probe; surface protein.	
XX		
OS	Neisseria meningitidis strain b2.	
XX		
FT	key	location/Qualifiers
FT	Peptide	1..19
FT	Protein	/label= sig_peptide
FT		20..174
XX		/label= mat_protein
PN	W09629412-A1.	
XX		
PD	26-SEP-1996.	
XX		
PF	15-MAR-1996;	96MO-CA00157.
XX		
PR	04-AUG-1995;	95US-0001983.
PR	17-MAR-1995;	95US-0406362.
XX		
PA	(IAFB-) IAF BIO VAC INC.	
XX		
PI	Brodeur BR, Hamel J, Martin D, Rioux C;	
XX		

E. coli cellular p
Salmonella typhi c
Virulence gene pro
Chlamydia trachoma
Virulence gene pro
Actinobacillus ple
Actinobacillus ple
Cysteine protease
M. catarrhalis str
N. meningitidis 60
Actinobacillus ple
All. protein-matlos
Arabidopsis thalia
M. catarrhalis str
M. catarrhalis str
M. catarrhalis str
Attachment-invasio
Helicobacter pylori
H. pylori bacteria
Proteinase K varia
Outer membrane pro
Protein associated
N. meningitidis 60
Arabidopsis thalia
Porphyromonas ging
H. pylori ORF 05ec
H. pylori ORF 05ec
Helicobacter pylori
H. pylori outer me
H. pylori outer me

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DR WPI: 1996-443187/44.
DR N-PSDB; AAT39042.
XX Neisseria meningitidis antigen, highly conserved between different
PT strains - useful for prodn. of antibodies for immunisation against,
PT or diagnosis of, N. meningitidis infection
XX
XX Claim 7; Fig 10; 117pp; English.
XX
CC A proteinase K resistant surface protein has been isolated
CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
CC 22 kd antigen, antigenic fragments of antibodies can be used
CC in a vaccine for the prevention of infection by N. meningitidis or
CC by N. gonorrhoeae in humans. The antibodies may also be used
CC diagnostically to detect N. meningitidis infection. The antigen
CC may also be used to detect antibodies specific to N. meningitidis
CC antigen.
CC DNA sequences encoding the antigen, or their fragments, can be used
CC as probes for the detection of pathogenic Neisseria bacteria.
CC
SQ Sequence 174 AA:
Query Match 100.0%; Score 870; DB 17; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.8e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKALALIALALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASVITDFQSPVYKPYFGARLSLNRAAHLGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASVITDFQSPVYKPYFGARLSLNRAAHLGSDSF 120
QY 121 SKTSAGIGVLAGSVYAVTPNVDLAGYRYNIVGKNTVKNVRSSELGAGYRVKF 174
DB 121 SKTSAGIGVLAGSVYAVTPNVDLAGYRYNIVGKNTVKNVRSSELGAGYRVKF 174

RESULT 2
AAM04893
ID AAM04893 standard; Protein; 174 AA.
XX
AC AAM04893;
XX
XX 22-DEC-1996 (first entry)
DE Proteinase K resistant N. meningitidis 22 kd surface protein.
XX
XX Proteinase K resistant; Neisseria meningitidis;
KM Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
XX
OS Neisseria meningitidis strain Z4063.
XX
XX Key Location/Qualifiers
XX FH Peptide 1..19
XX FT /label= sig_peptide
XX FT Protein 20..174
XX FT /label= mat_protein
XX
XX WO9629412-A1.
XX
XX 26-SEP-1996.
XX
XX 15-MAR-1996; 96WO-CA00157.
XX
XX 04-AUG-1995; 95US-0001983.
XX 17-MAR-1995; 95US-0406362.
XX
XX (IAFB-) IAF BIO VAC INC.
XX
XX Brodeur BR, Hamel J, Martin D, Rioux C;
XX

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DR WPI: 1996-443187/44.
DR N-PSDB; AAT39041.
XX Neisseria meningitidis antigen, highly conserved between different
PT strains - useful for prodn. of antibodies for immunisation against,
PT or diagnosis of, N. meningitidis infection
XX
XX Claim 7; Fig 9; 117pp; English.
XX
CC A proteinase K resistant surface protein has been isolated
CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
CC 22 kd antigen, antigenic fragments of antibodies can be used
CC in a vaccine for the prevention of infection by N. meningitidis or
CC by N. gonorrhoeae in humans. The antibodies may also be used
CC diagnostically to detect N. meningitidis infection. The antigen
CC may also be used to detect antibodies specific to N. meningitidis
CC antigen.
CC DNA sequences encoding the antigen, or their fragments, can be used
CC as probes for the detection of pathogenic Neisseria bacteria.
CC
SQ Sequence 174 AA:
Query Match 95.9%; Score 834; DB 17; Length 174;
Best Local Similarity 95.4%; Pred. No. 2.7e-81;
Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 MKKALALIALALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASVITDFQSPVYKPYFGARLSLNRAAHLGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASVITDFQSPVYKPYFGARLSLNRAAHLGSDSF 120
QY 121 SKTSAGIGVLAGSVYAVTPNVDLAGYRYNIVGKNTVKNVRSSELGAGYRVKF 174
DB 121 SKTSAGIGVLAGSVYAVTPNVDLAGYRYNIVGKNTVKNVRSSELGAGYRVKF 174

RESULT 3
AAM04891
ID AAM04891 standard; Protein; 174 AA.
XX
AC AAM04891;
XX
XX 22-DEC-1996 (first entry)
DE Proteinase K resistant N. meningitidis 22 kd surface protein.
XX
XX Proteinase K resistant; Neisseria meningitidis;
KM Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
XX
OS Neisseria meningitidis strain 608B.
XX
XX Key Location/Qualifiers
XX FH Peptide 1..19
XX FT /label= sig_peptide
XX FT Protein 20..174
XX FT /label= mat_protein
XX
XX WO9629412-A1.
XX
XX 26-SEP-1996.
XX
XX 15-MAR-1996; 96WO-CA00157.
XX
XX 04-AUG-1995; 95US-0001983.
XX 17-MAR-1995; 95US-0406362.
XX
XX (IAFB-) IAF BIO VAC INC.
XX
XX Brodeur BR, Hamel J, Martin D, Rioux C;
XX

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DR WPI: 1996-443187/44.
 DR N-PDB: AAT39039.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 1; 117pp; English.
 XX
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 XX
 SQ Sequence 174 AA:

Query Match 94.8%; Score 825; DB 17; Length 174;
 Best Local Similarity 94.3%; Pred. No. 2,5e-80;
 Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKKALALIALPALPAALAEAGSGFYQADAAHAKASSLSGKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPALPAALAEAGSGFYQADAAHAKASSLSGKGFSPRISAGYRINDLR 60
 QY 61 FAVDTTRKKNKAPSTDKRLYSIGASVLYIDPTOSPVKPYGKARLSLNRAAHLCGSDS 120
 DB 61 FAVDTTRKKNKAPSTDKRLYSIGASVLYIDPTOSPVKPYGKARLSLNRAAHLCGSDS 120
 QY 121 SKTSAGLGLVLAGSVAVTPNVLDAGRYRYNKGKNTYKRVNRSGLSAGVRVKE 174
 DB 121 SGTSTGLGLVLAGSVAVTPNVLDAGRYRYNKGKNTYKRVNRSGLSAGVRVKE 174

RESULT 4

AAW04892
 ID AAW04892 standard; Protein; 175 AA.

XX
 AC AAW04892;
 XX
 DT 22-DEC-1996 (first entry)
 XX
 DE Proteinase K resistant N. meningitidis 22 kD surface protein.
 XX
 KM Proteinase K resistant; Neisseria meningitidis;
 KM Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
 XX
 OS Neisseria meningitidis strain MCH88.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= s1g-peptide
 FT 20..175
 FT Protein /label= mat_protein
 XX
 PN W09629412-A1.
 PD 26-SEP-1996.
 XX
 PF 15-MAR-1996; 96WO-CA00157.
 XX
 PR 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 XX
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 DR N-PDB: AAT39040.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 8; 117pp; English.
 XX
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 XX
 SQ Sequence 175 AA:

Query Match 93.5%; Score 813.5; DB 17; Length 175;
 Best Local Similarity 93.7%; Pred. No. 4.3e-79;
 Matches 164; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 MKKALALIALPALPAALAEAGSGFYQADAAHAKASSLSGKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPALPAALAEAGSGFYQADAAHAKASSLSGKGFSPRISAGYRINDLR 60
 QY 61 FAVDTTRKKNKAPSTDKRLYSIGASVLYIDPTOSPVKPYGKARLSLNRAAHLCGSDS 119
 DB 61 FAVDTTRKKNKAPSTDKRLYSIGASVLYIDPTOSPVKPYGKARLSLNRAAHLCGSDS 120
 QY 120 FSKTSAGLGLVLAGSVAVTPNVLDAGRYRYNKGKNTYKRVNRSGLSAGVRVKE 174
 DB 121 FSKTSAGLGLVLAGSVAVTPNVLDAGRYRYNKGKNTYKRVNRSGLSAGVRVKE 175

RESULT 5

AAAB19895
 ID AAB19895 standard; Protein; 155 AA.

XX
 AC AAB19895;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE Neisseria meningitidis NSPA protein.
 XX
 KM NSPA; infection; diagnosis; therapy; vaccine; meningococcal B.
 KM Neisseria meningitidis.
 XX
 OS Neisseria meningitidis.
 XX
 FH Key Location/Qualifiers
 FH Region 6..17
 FT /note= "transmembrane beta-strand"
 FT 18..26
 FT /note= "surface-exposed connecting loop"
 FT 27..37
 FT /note= "transmembrane beta-strand"
 FT 40..50
 FT /note= "transmembrane beta-strand"
 FT 51..62
 FT /note= "surface-exposed connecting loop"
 FT 63..74
 FT /note= "transmembrane beta-strand"
 FT 78..88
 FT /note= "transmembrane beta-strand"
 FT 89..104
 FT /note= "surface-exposed connecting loop"
 FT 105..114
 FT /note= "transmembrane beta-strand"
 FT 118..130
 FT Region

```

FT      /note= "transmembrane beta-strand"
FT      Region      131..145
FT      /note= "surface-exposed connecting loop"
FT      Region      146..155
FT      /note= "transmembrane beta-strand"
XX      WO200071725-A2.
XX      30-NOV-2000.
XX      19-MAY-2000; 2000MO-IB00828.
XX      19-MAY-1999; 99GB-0011692.
XX      19-AUG-1999; 99GB-0019705.
XX      09-MAR-2000; 2000GB-0005730.
XX      (CHIR-) CHIRON SPA.
XX      Giuliani MM, Pizsa M, Rappuoli R;
XX      WPI; 2001-025167/03.
XX      Novel composition comprising first and second biological molecules from
XX      a Neisseria bacterium, useful as vaccines or immunogenic compositions
XX      for treating Neisserial infections
XX      Example 12; Fig 32; 126pp; English.
XX      The present sequence is that of the Neisseria meningitidis Nspa
XX      protein, which contains 8 transmembrane beta-strands and 4
XX      surface-exposed connected loops. Recombinant Nspa is being
XX      developed as a vaccine for the prevention of meningococcal
XX      disease caused by all serotypes. The invention provides
XX      combination compositions comprising: (i) 2 or more Neisserial
XX      proteins, (ii) 2 or more different Neisserial nucleic acids; or
XX      (iii) mixtures of 1 or more Neisserial protein and 1 or more
XX      Neisserial nucleic acid. The proteins and nucleic acids are
XX      preferably from different Neisseria spp., especially Neisseria
XX      meningitidis and Neisseria gonorrhoeae, but may be from the same
XX      species. A claimed composition includes the Nspa protein,
XX      preferably in mature form. The compositions are used e.g. as
XX      immunogenic compositions, vaccines or diagnostic reagents. They
XX      are used to treat or prevent Neisserial infection, to detect the
XX      presence of Neisserial bacteria or of antibodies raised against
XX      Neisserial bacteria, and/or as reagents which can raise antibodies
XX      against Neisserial bacteria.
XX      Sequence      155 AA:
SQ      Query Match      85.9%; Score 747; DB 22; Length 155;
      Best Local Similarity 94.2%; Pred. No. 4.8e-72;
      Matches 146; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
OY      20 EGAGGFVVOADAHAHAKASSLSGKSPRISAGYRINDLRFVNDTRYKNYKAPSTDRK 79
      |||||||
DB      1 EGAGGFVVOADAHAHAKASSLSGKSPRISAGYRINDLRFVNDTRYKNYKAPSTDRK 60
OY      80 LYSIGASVIYDFDQSPVKPYFGARLSLNRSASHLGGSDSFSKTSAGLGVLAGSYAVMP 139
      |||||||
DB      61 LYSIGASVIYDFDQSPVKPYFGARLSLNRSASVDLGGSDSFSKTSAGLGVLAGSYAVMP 120
OY      140 NVDLADAGRYNYGKVTYKNNVSGELSGAGYRYKF 174
      |||||||
DB      121 NVDLADAGRYNYGKVTYKNNVSGELSGAGYRYKF 155

```

RESULT 6
AAW04912
ID AAW04912 standard; Protein; 25 AA.

AC AAW04912;
XX
XX 22-DEC-1996 (first entry)

```

XX      N. meningitidis 608B peptide CS-857.
DE      XX
XX      Proteinase K resistant; Neisseria meningitidis; epitope; mapping;
XX      Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
XX      Synthetic.
XX      WO9629412-A1.
XX      26-SEP-1996.
XX      15-MAR-1996; 96WO-CA00157.
XX      04-AUG-1995; 95US-0001983.
XX      17-MAR-1995; 95US-0406362.
XX      (IAFB-) IAF BIO VAC INC.
XX      Brodeur BR, Hamel J, Martin D, Rioux C;
XX      WPI; 1996-443187/44.
XX      Neisseria meningitidis antigen, highly conserved between different
XX      strains - useful for prodn. of antibodies for immunisation against,
XX      or diagnosis of, N. meningitidis infection
XX      Claim 24; Page 84; 117pp; English.
XX      Example 9 describes the epitope mapping of the 22 kD
XX      N. meningitidis protein. Identification was accomplished
XX      using 18 overlapping synthetic peptides (AAW04895 to AAW04912).
XX      Sequence      25 AA:
SQ      Query Match      15.3%; Score 133; DB 17; Length 25;
      Best Local Similarity 100.0%; Pred. No. 2.3e-07;
      Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      61 FAVDYTRYKNYKAPSTDRKLYSIGA 85
      |||||||
DB      1 FAVDYTRYKNYKAPSTDRKLYSIGA 25

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RESULT 7
ID AAR73911 standard; protein; 170 AA.

AC AAR73911;

DT 05-DEC-1995 (first entry)

DE Neisseria meningitidis opacity related protein POPM3.

KM Neisseria meningitidis; opacity related protein POPM3; vaccine;

KM meningitidis related homologous antigenic sequence; MRHA5; RV-1;

KM immunosay; diagnosis; treatment; prophylactic; bacterial;

OS Neisseria meningitidis.

PN WO9509232-A.

PD 06-APR-1995.

PF 28-SEP-1994; 94WO-CA00516.

PR 28-SEP-1993; 93US-0127499.

XX (SHAR/) SHARMA L R.

PA (VALS/) VAN ALSTYNE D.

XX Sharma LR, Van Alstyne D;

XX DR WPI: 1995-147431/19.

XX DR New peptide(s) and corresp. antibodies for the treatment of

PT meningitis - the peptide(s) corresp. to homologous antigenic

PT sites on bacterial and viral agents and on chemokine(s), used for

PT detecting and preventing meningitis

XX PS Claim 47; Fig 5/10; 98pp; English.

XX AA AAR73911 is the *Neisseria meningitidis* opacity related protein POPM3.

CC It contains the meningitis related antigenic sequences (MRHAs)

CC claimed in AAR73889 and AAR73901, which are recognised by a monoclonal

CC antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAs

CC peptides may be used in immunoassays to diagnose the presence of

CC bacterial and/or viral meningitis agents in a sample, or in

CC prophylactic and therapeutic meningitis treatments. The peptides may

CC NB: Identified by matching corresponding MRHAs peptides.

XX Sequence 170 AA;

XX Query Match 14.4%; Score 125; DB 16; Length 170;

Best Local Similarity 25.2%; Pred. No. 2.2e-05;

Matches 37; Conservative 18; Mismatches 46; Indels 46; Gaps 3;

QY 6 AALIALPALPAALAEAGSGFYVQADAAH-----AKASSLSG-----AKG 45

DB 15 SSLFSSAAQAASBDRKSPYVQADLAYAARITHYPOATGANNSTVSDYFNRIRAS 74

QY 46 FSPRISAGYRINDRFANDYTRYKNY-----KAPSTDFK 79

DB 75 IHPRVSGYDYGGMRIADYASYRKMNNKYSVTKLEKNKDKLKTENDENGTFPHA 134

QY 80 LYSIGASYTYDPTQSPYKPYFGARLS 106

DB 135 ASSIGLSAIYDFKLGKFKRYIGARVA 161

RESULT 8

AAAB47447

ID AAB47447 standard; Protein: 353 AA.

XX AC AAB47447;

XX DT 31-OCT-2001 (first entry)

XX DE MOMP P5.

XX KM surface exposed loop; major outer membrane protein P5; MOMP P5;

KW non-typable H. influenzae; nH1; IBI(f) peptide; B cell epitope;

KW otitis media; sinusitis; conjunctivitis;

KW lower respiratory tract infection.

XX OS Haemophilus influenzae.

XX FH Key

FT Location/Qualifiers

FT 38..57

FT /label= Loop 1

FT /note= "Extracellular domain"

FT 89..100

FT /label= Loop 2

FT /note= "Extracellular domain"

FT 136..150

FT /label= Loop 3

FT /note= "Extracellular domain"

FT 181..204

FT /label= Loop 4

FT /note= "Extracellular domain"

XX PN MO200161013-A1.

XX PD 23-AUG-2001.

XX PF 13-FEB-2001; 2001WO-EP01556.

XX PR 15-FEB-2000; 2000GB-0003502.

XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Berthet FJ, Denoel P, Poolman J, Thonnard J;

XX DR WPI: 2001-52259/57.

XX PT Recombinant bacterial outer membrane protein where one or more

PT surface-exposed loops are modified is useful as a vaccine to prevent or

PT treat Haemophilus influenzae infection or associated disease, e.g.,

PT otitis media and conjunctivitis -

XX PS disclosure; Fig 1, 29pp; English.

XX CC This sequence represents the major outer membrane protein P5 of

CC non-typable H. influenzae. One or more surface exposed loops of this

CC protein may be replaced with a modified peptide of the invention. Each

CC of these peptides contain an IBI(f) peptide which is a 19 amino acid

CC peptide derived from the sequence of MOMP P5 from strain nH1128

CC representing amino acids Arg117 to Gly135. This peptide represents the

CC third exposed loop of P5 and is a potential B cell epitope. The loops

CC of the invention are modified in terms of being in a non-native

CC environment in the recombinant outer membrane protein. The modified

CC MOMP P5 may be used to induce an immune response in a mammal to

CC prevent or treat Haemophilus influenzae infection or associated

CC disease, e.g., otitis media, sinusitis, conjunctivitis, or lower

CC respiratory tract infection.

XX SQ Sequence 353 AA;

XX Query Match 12.2%; Score 106; DB 22; Length 353;

Best Local Similarity 25.2%; Pred. NO. 0.0063;

Matches 54; Conservative 30; Mismatches 90; Indels 40; Gaps 9;

QY 1 MKKALALALALPAALAEAG---SGFYVQADAAHAKASSLSG-----AKGPS 47

DB 1 MKKTALALVAGLAASVQAAPQENTFYAGVKAQASPHDLRALARKYKGYHRNSTY 60

QY 48 PRISAGYRINDRFANDYTRYKNYKAPSTDFKLYSIGA--SVIYDPTQSPV 97

DB 61 YGVFGGYOILNONNLGLAVELGYDFGRAGKREKTVYKHTNHGTHSLKSGYVLEGL 120

QY 98 KPYFGARLSINRASAHLSGSDSPSKTSAG-----IGVLA-CGVSAVAPPNVDLAGY-- 147

DB 121 DYGKAGVALVNSDYKLYENSSSTLKKLGEHHRARASGLFAVGAELVAPLPAVLEIYQW 180

QY 148 ----RYNVYGVKVNPKVNRYS--GELSGAVRYKF 174

DB 181 LTRVGYRQDKRNTALNPNWIGSINAGISYRF 214

RESULT 9

AAAR66294

ID AAR66294 standard; Protein: 359 AA.

XX AC AAR66294;

XX DT 09-AUG-1995 (first entry)

XX DE Non-typable Haemophilus influenza (NTHi) fimbria protein.

XX KM Fimbria protein; vaccine; otitis media.

XX OS Haemophilus influenza strain 1128.

XX FH Key

FT Location/Qualifiers

FT 22..33

FT /label= amino terminus

FT Peptide 234..249

/label= internal CNBR fragment

FT XX MO9426304-A.
 PN XX
 XX XX
 PD 24-NOV-1994.
 XX XX
 PF 12-MAY-1994; 94WO-US05477.
 XX XX
 PR 18-MAY-1993; 93US-0065442.
 XX XX
 PA (OHIO-) OHIO STATE RES FOUND.
 PI Bakaletz LO, Kolattukudy PE, Strakova T;
 XX XX
 DR WPI; 1995-006359/01.
 DR N-PSDB; AAQ78916.
 PT Vaccine comprising non-typable Haemophilus influenza fimbria
 PT protein - useful in studying, preventing or reducing the
 PT severity of otitis media, also fimbria protein and DNA.
 XX XX
 PS Disclosure; Fig 5; 45pp; English.
 CC The fimbria proteins from 15 randomly selected type b and non-
 CC typable clinical isolates of Haemophilus influenza share common
 CC epitopes. Thus fimbria isolated from non-typable Haemophilus
 CC influenzae 1128 strain is a particularly suitable immunogen to
 CC protect against the different non-typable Hf. influenzae that cause
 CC otitis media. Fimbria protein is produced by culturing a transformed
 CC microbial host, pref. E.coli, Sporodoptera frugiperda or a mucosal
 CC pathogen. Fimbria protein (FP) produced by this process is claimed.
 CC The FP protein migrates in polyacrylamide gels to a posn. equiva. to
 CC a mol. wt. of 25.5 kD or 37.5 kD.
 XX XX
 SQ Sequence 359 AA;

Query Match 11.6%; Score 101; DB 16; Length 359;
 Best Local Similarity 25.1%; Pred. No. 0.022;
 Matches 57; Conservative 27; Mismatches 83; Indels 60; Gaps 12;

QY 1 MKKALALIALALPAAALAEGA---SGFYQADAA---HAKSSSLGSAKSPRISAG 53
 DB 1 MKKTATLALVYAGLAAASVAAAPQENTFYAGYVAGSGSHDGINNGAATKGLSS-NTG 59
 QY 54 YRINDLFAVDYRKYRKYKAPSTDFKLYSIGASVIY-DF---DTQSPVP-----YFGAR 104
 DB 60 YRNTFTYGV---FGGYQLNQD--NFGLAELGYHDEGRAKLRAGKPKKHTNHGAY 113
 QY 105 LSLNRSAHLGSGDSFSKTSAGL-----GVLG-GVSYA 136
 DB 114 LSLKGSYEVLGDLVYGKAGVALVRSDYKFEEDANGTRDHKKGRHTRARASGLFAVGALEYA 173
 QY 137 VTENNVDLAGY-----RYNYGKVTYKVNYS--GELSAGRYKF 174
 DB 174 VLPELAVRLEYQWLTVRGKTRPODKPENTATINPMIGICINAGISTRF 220

RESULT 10
 AA97900
 ID AA97900 standard; protein; 369 AA.
 AC AA97900;
 XX XX
 DT 19-DEC-2000 (first entry)
 XX XX
 DE Actinobacillus pleuropneumoniae OmpA2.
 XX XX
 KW Outer membrane protein; OmpA1; vaccine; pig; immunogen;
 XX dual immune response; immunogen; pleuropneumonia.
 OS Actinobacillus pleuropneumoniae.
 XX XX
 PN EP105133-A2.

XX XX 13-SEP-2000.
 PD PD
 XX XX
 PF 14-FEB-2000; 2000EP-0301103.
 XX XX
 PR 17-FEB-1999; 99US-0120454.
 XX XX
 PA (PFIZ) PFIZER PROD INC.
 XX XX
 PI Campos M, Martindale SR, Dutschi BA, Yule TD;
 DR WPI; 2000-566924/53.
 XX XX
 PT Novel fusion protein for producing a dual immune response comprises a
 PT peptide analogous to an endogenous peptide which is to be inhibited,
 PT connected to a peptide analogous to an immunogen from a pathogen which
 PT infects a vertebrate -
 XX XX
 PS Disclosure; Page 58-60; 93pp; English.
 CC The present sequence is that of outer membrane protein OmpA2 of
 CC Actinobacillus pleuropneumoniae. OmpA2 can be utilized in fusion
 CC proteins of the invention that are used as vaccines eliciting a
 CC dual immune response. Such fusion proteins comprise: a first
 CC protein that is endogenous to a vertebrate, and the activity of which
 CC is to be inhibited within the vertebrate, and which is incapable by
 CC itself of eliciting an effective immunoinhibitory response in the
 CC vertebrate; and a second protein, which is an immunogen from a
 CC pathogen capable of infecting the vertebrate, and which causes the
 CC vertebrate's immune system to recognise the first protein,
 CC producing a response that inhibits the activity of the first
 CC protein, and also protecting the vertebrate from infection by the
 CC pathogen when the vertebrate is vaccinated with the fusion protein.
 CC In the present case, a fusion protein of cholera toxin and OmpA2
 CC is useful for encouraging appetite in swine while simultaneously
 CC providing a protective immune response against porcine
 CC pleuropneumonia.
 XX XX
 SQ Sequence 369 AA;

Query Match 11.0%; Score 96; DB 21; Length 369;
 Best Local Similarity 23.6%; Pred. No. 0.078;
 Matches 55; Conservative 29; Mismatches 81; Indels 68; Gaps 13;

QY 1 MKKALALIALALPAAALAEGA---SGFYQADAAHAKSSSLGSAK-GSPR----- 49
 DB 1 MKKSIVLALVLS--AAAVQAAPQONTFYAGAKYGGSPFHGVQLKSGHDDRNKTRK 58
 QY 50 -----ISAGYRI--NDLFAVD--YTRYKMYKAPSTDFKLYSIGA----- 85
 DB 59 YGINRNSVTYGVFGGYQLNQDNNGLATELGYDYGVRGNDGBFRAMKHSAGLNFALK 118
 QY 86 ---SVYDFEDYQSPYKPFYFARLSLNRASAHLG-----SDSSKTSAGLGVYAGSYA 136
 DB 119 PSYEVLPLDLYGKV---GVAVVRNDYKSY-GAENTNEPTEKFKUKASTTIGAGLEYA 173
 QY 137 VTENNVDLAGYRYNYGKVTYKVN--VRSQ-----ELSGAVRYKF 174
 DB 174 ILP--ELAAVRYEYQWLTVRGKTRPODKPENTATINPMIGICINAGISTRF 224

RESULT 11
 AA97900
 ID AA97900 standard; protein; 369 AA.
 AC AA97900;
 XX XX
 DT 11-SEP-2000 (first entry)
 XX XX
 DE Actinobacillus pleuropneumoniae outer membrane protein, OmpA2.
 XX XX
 KW OmpA2; outer membrane protein; APP; pneumonic pathogen; swine;
 XX sus scrofa; serotype; antigen; vaccine; cross-reactive immunity;

KM cross-protection; diagnosis.
 OS Actinobacillus pleuropneumoniae strain Pz420.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /note="Signal peptide"
 FT Protein /note="Mature OmpA2"
 XX
 PN EPI001025-A2.
 XX
 PD 17-MAY-2000.
 XX
 PF 20-OCT-1999; 99EP-0308262.
 XX
 PR 22-OCT-1998; 98US-0105285.
 XX
 PA (PEITZ) PEITZER PROD INC.
 XX
 PI Ankenbauer RG, Baarsch MJ, Campos M, Reich RL, Rosey EL;
 PI Warren-Stewart LM, Sulter BT;
 XX
 DR MPI; 2000-320438/28.
 DR N-PSDB; AAA38558.
 XX
 PT Low molecular weight Actinobacillus pleuropneumoniae proteins and DNA
 PT encoding them, for use as vaccines against the bacteria in swine -
 XX
 PS Claim 2; Fig 5; 81pp; English.
 XX
 CC This sequence represents a low molecular weight outer membrane
 CC protein, OmpA2, from Actinobacillus pleuropneumoniae (APP) strain
 CC Pz420 (ATCC 98930). The invention relates to the novel APP outer
 CC membrane proteins Omp20, OmpW, Omp27, OmpA1 and OmpA2 (AAV97896-Y97900)
 CC and to nucleic acids encoding them (AAA38554-A38558). APP is a Gram
 CC negative coccobacillus which is one of the most important swine
 CC pneumonia pathogens. 12 different serotypes of APP have been recognised
 CC which vary in geographic distribution. Prior art attempts at vaccinating
 CC against APP have produced mainly serotype-specific immune responses. In
 CC contrast, natural immunity to any one serotype seems to confer
 CC significant protection from disease caused by other serotypes, suggesting
 CC that natural exposure induces cross-reactive immunity to shared antigens.
 CC The novel outer membrane proteins of the invention are present in all 12
 CC serotypes, and may provide a target for cross-protective immunisation.
 CC The novel outer membrane proteins and nucleic acids encoding them can be
 CC used as a vaccine against APP in swine. They can also be used as
 CC reagents for the diagnosis of APP infections.
 CC
 XX
 SQ Sequence 369 AA;
 Query Match 11.0%; Score 96; DB 21; Length 369;
 Best Local Similarity 23.6%; Pred. No. 0.078;
 Matches 53; Conservative 29; Mismatches 81; Indels 68; Gaps 13;
 OY 1 MKKALALIALALPAALALEGA---SGFYVQADAAHAKASSISGSAK-GFSPR----- 49
 DB 1 MKKSLVALAVLS--AAVAQAAPQONTFAAGAKVQSSHHGVNQLKSHDRIYMDKTRK 58
 OY 50 -----ISAGYRI--NDLRFAYD--YTRYKNYKAPSTDPLKXYSIGA----- 85
 DB 59 YGINRNSVTYGVFGGYOILNQNNGFLATELGYDYGRVANGGERFRAMKSHSHGLNPAALK 118
 OY 86 ---SVYDEPDQSPVKPYRGARLSLNRSAHLGG-----SSSEKTSAGLGVLAGVSYA 136
 DB 119 PSYEVLDPDLDVYGVKY---GVAVVRNDYKSY-GAENTNEPTEKFRKLASTILGAGVEYA 173
 OY 137 VTPNVDLDAGYRYNYGVKNYTKN--VRSG-----EISAGYRVAF 174
 DB 174 ILP--ELARVEYQYLKNGKGNLAKALVRSCTQDDVDFQYAPADLHSTYAGLSYRF 224
 RESULT 12

AAU34556
 ID AAU34556 standard; Protein; 212 AA.
 XX
 AC AAU34556;
 XX
 DT 14-FEB-2002 (first entry)
 DE
 XX E. coli cellular proliferation protein #137.
 XX
 KM Antisense; prokaryotic cellular proliferation protein;
 KM antibiotic; antibacterial; drug design.
 XX
 OS Escherichia coli.
 XX
 PN WO2001/0955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELITT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
 PI Yamamoto RT, Xu HH;
 XX
 DR MPI; 2001-611495/70.
 DR N-PSDB; AAS52415.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Example 3; Seq ID No 10149; 51pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 212 AA;
 Query Match 11.0%; Score 95.5; DB 22; Length 212;
 Best Local Similarity 23.8%; Pred. No. 0.042;
 Matches 49; Conservative 26; Mismatches 72; Indels 59; Gaps 10;
 OY 1 MKKALALIALAL--LPAALALEGSGFYVQADAAHAK---ASSISGSAKGFSPRISAGY 54
 DB 1 MKKLTVALAVLTLLSGSAFAHGEFFMRAGSATVPTFGAGTGLSGLGGSFYV----- 54
 OY 55 RINDLRFAYDYTRYKNKA-----PSTDPLKXISGASVLYDF----- 91

Db 55 -TNNQGLGLET---YMATDNIGVELLAATPFR-HKIGTRATCDIATVHHLPPTLMAQW 108
 Qy 92 ---DTOSPKRPFEGARLS-----LNRAAHGSGDSFSTSGAGLGVAGSYAVTPN 140
 Db 109 YFGDASSKRPYPYAGAGINTTFFPDNGFNDHCKEAGLSDLSKDSWGAAGQGVYDLINRD 168
 Qy 141 --VDLDAGYRNYGVKNTVKNVRSRSG 164
 Db 169 WLVMMSVWYM-----DIDTTANYKLG 189

RESULT 13
 AAU38252
 ID AAU38252 standard; Protein; 257 AA.
 AC AAU38252;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Salmonella typhi cellular proliferation protein #143.
 XX
 KM Antisense; prokaryotic cellular proliferation protein;
 KM antidiotic; antibacterial; drug design.
 XX
 OS Salmonella typhi.
 XX
 PN WO200170955-A2.
 PD 27-SEP-2001.
 XX
 PE 21-MAR-2001; 2001WO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr CJ;
 PI Yamamoto RT, Xu HH;
 XX
 DR MPI; 2001-611495/70.
 DR N-PSDB; AAS56111.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 PS
 PS Example 3; seq ID No 13845; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 257 AA;
 Query Match 10.9%; Score 95; DB 22; Length 257;
 Best Local Similarity 24.1%; Pred. No. 0.062;
 Matches 54; Conservative 26; Mismatches 78; Indels 66; Gaps 12;

Qy 1 MKKALALIALA--LPAALAEAGSGFYQADAHAHAK-----ASSISGASAKGSPRISAGY 54
 Db 27 MKKFTVALALTTLLSGSAFHEAGFEFFMRAGPATVPTGAGGTGLHNGFD--VS--- 81
 Qy 55 RINDLRFVVDYTRKKNKA-----PSTDFLYSIGASVYDF----- 91
 Db 82 --TNNQGLGLET---YMATDNIGVELLAATPFR-HKVGATGADIAVHLPPTLMAQW 134
 Qy 92 ---DTOSPKRPFEGARLS-----LNRAAHGSGDSFSTSGAGLGVAGSYAVTPN 140
 Db 135 YFGDSSSKRPYPYAGVNYTFFPDNDFNDGKKTGTLSDLSFKDSXGAAGQGVYDLINRD 194
 Qy 141 -----VDLDAGYRNYGVKNTVKNVRSRSG-----LSAGVR 171
 Db 195 WLIGASVWYMDIDTTANYK-MGVOQHDVSRLDPWVEMFSKGR 237

RESULT 14
 AAB44589
 ID AAB44589 standard; Protein; 369 AA.
 AC AAB44589;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Virulence gene protein #69.
 XX
 KM Virulence gene; antibacterial; vaccine; bacterial infection;
 KM septicemia; bronchopneumonia; rhinitis; wound infection.
 XX
 OS Actinobacillus pleuropneumoniae.
 XX
 PN WO200061724-A2.
 XX
 PD 19-OCT-2000.
 XX
 PE 06-APR-2000; 2000WO-US09218.
 XX
 PR 09-APR-1999; 99US-0128689.
 PR 10-SEP-1999; 99US-0153453.
 XX
 PA (PHAA) PHARMACIA & UPJOHN INC.
 XX
 PI Lowery DE, Fuller TE, Kennedy MJ;
 PI
 XX
 DR MPI; 2000-647422/62.
 DR N-PSDB; AAC79664.
 XX
 PT Attenuated Pasteurellaceae bacteria comprising mutations in virulence
 PT genes, useful as a live attenuated vaccine against bacterial infections
 PS
 PS Claim 39; Pages 308-309; 322pp; English.
 XX
 CC The family Pasteurellaceae encompasses several pathogens that infect a
 CC wide variety of animals. The present invention relates to virulence genes
 CC from Pasteurellaceae. The present sequence is a protein encoded by one
 CC such virulence gene. The virulence genes of the present invention may be
 CC mutated in order to produce an inactive gene. The inactive virulence gene
 CC may in turn be used to produce a vaccine, which is useful for treating
 CC bacterial infections such as septicemias, bronchopneumonias, rhinitis and
 CC wound infections.
 CC
 CC Sequence 369 AA;
 SO

Query Match 10.9%; Score 95; DB 21; Length 369;
 Best Local Similarity 24.2%; Pred. No. 0.1;

Matches 57; Conservative 27; Mismatches 78; Indels 74; Gaps 14;

QY 1 MKRALALALALPAAALAECA---SGEYVQADAAHAKASSLSGAK-GFSPR----- 49
 Db 1 MKSLVALAVLS---AAVNAQAPQONTFYGAHVGGSSFHGYNQJLKGDDHXYNKRTR 58
 QY 50 -----ISAGRI---NDLRFADV---YTRYKNYKAPSDFKLYSTGA----- 85
 Db 59 YGINRNSVTYGVFGYOILNQNNGELAAELGYDYGRVGRNVDFFRTVKHSAHGLNLALR 118
 QY 86 ---SVYDEPTQSPV-----KPYFGARLSLNRASAHLSGSDSFSTSLGLVLAGV 133
 Db 119 PSYEVLPLDLVYGVKGLAVVRNDYKRY-GAE-NTNESTT-----KFKLKASTYILGAGV 170
 QY 134 SYAVTFVNDLDAGIRINYGVKNTVRN--VRSG-----ELSGAVRVKF 174
 Db 171 EYALLP--ELAAVVEYOYLNKAGNLKALVRSCTQVDVDFQYAPDIRHVTAGLSYRF 224

RESULT 15

AAV36955

ID AAV36955 standard; Protein; 797 AA.

XX AAY36955;

DT 07-OCT-1999 (first entry)

DE Chlamydia trachomatis surface exposed protein.

XX

KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 paratrachoma; inclusion conjunctivitis; genital disease; perinephritis;
 nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
 bartholinitis; pneumopathy; venereal lymphogranulomatosis.

KM Chlamydia trachomatis.

OS WO9928475-A2.

PN 10-JUN-1999.

PD 27-NOV-1996; 98WO-IB01939.

PF 04-NOV-1998; 98US-0107077.

PR 28-NOV-1997; 97ER-0015041.

PR 17-DEC-1997; 97ER-0016034.

XX (GEST) GENSET.

XX Griffiths R;

DR WPI; 1999-371125/31.

PT Genome sequence of Chlamydia trachomatis

PS Disclosure; Page 802; 1755pp; English.

AAV36754-Y37949 are encoded by open reading frames (ORFs) of the genome
 of Chlamydia trachomatis (see AAY01425). The polypeptides can be used as
 vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
 can also be used to control growth of the microorganism. Chlamydia
 trachomatis is responsible for a large number of diseases, e.g. eye
 diseases such as conventional trachoma, nonendemic trachoma,
 paratrachoma, and inclusion conjunctivitis; genital diseases such as
 nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
 perinephritis, bartholinitis; pneumopathy in breast feeding infants;
 and venereal lymphogranulomatosis. The polypeptides of the invention
 may be of use in treating these diseases.

SQ Sequence 797 AA;

Query Match 10.9%; Score 94.5; DB 20; Length 797;

Best Local Similarity 29.6%; Pred. No. 0.32; Mismatches 34; Conservative 16; Indels 17; Gaps 4;

QY 27 VQADAAHAKASSLSGAKGFSPRISAGYRIND-LRFADV-----TRYKNYKA 73
 Db 522 VELDKSINKALSKDYSDVYGGNISTTYILNDKLYGMYGSGQTSLSLRKKTSSNRLG 581
 QY 74 PSTDFK---LYSIGASVIYDEPTQSPVRFPGARLSLNRASAHLSGSDSFSTSL 125
 Db 582 PLDSNKGTFVSAAGLNLVD-SIDNPKRPTMGIRSFNLXKELSGLGTYQPTKLT 635

Search completed: October 28, 2002, 16:00:40
 Job time : 25.7145 secs

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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:58:54 ; Search time 9.48637 seconds
(without alignments)
448.017 Million cell updates/sec

Title: US-09-684-883-8

Perfect score: 870
Sequence: 1 MKKALALALALPAALAE.....VNTKVRSGELSGVRKF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	870	100.0	174 4	US-08-913-362-8 Sequence 8, Appl1
2	834	95.9	174 4	US-08-913-362-6 Sequence 6, Appl1
3	825	94.8	174 4	US-08-913-362-2 Sequence 2, Appl1
4	823.5	94.7	175 4	US-08-913-362-30 Sequence 30, Appl1
5	813.5	93.5	175 4	US-08-913-362-4 Sequence 4, Appl1
6	133	15.3	25 4	US-08-913-362-26 Sequence 26, Appl1
7	125	14.4	170 1	US-08-127-499A-20 Sequence 20, Appl1
8	125	14.4	170 1	US-08-482-847-20 Sequence 20, Appl1
9	104	12.0	359 1	US-08-457-997B-2 Sequence 2, Appl1
10	104	12.0	359 1	US-08-467-722A-2 Sequence 2, Appl1
11	87.5	10.1	573 4	US-09-336-447A-3 Sequence 3, Appl1
12	87	10.0	16 4	US-08-913-362-15 Sequence 15, Appl1
13	86	9.9	568 5	PCT-US95-13749-5 Sequence 5, Appl1
14	83	9.5	610 4	US-09-336-447A-11 Sequence 11, Appl1
15	83	9.5	624 4	US-09-336-447A-7 Sequence 7, Appl1
16	83	9.5	889 4	US-09-336-447A-15 Sequence 15, Appl1
17	80	9.2	15 4	US-08-913-362-23 Sequence 23, Appl1
18	80	9.2	409 4	US-09-066-046-31 Sequence 31, Appl1
19	80	9.2	15 4	US-08-913-362-14 Sequence 14, Appl1
20	78	9.0	15 4	US-08-913-362-16 Sequence 16, Appl1
21	78	9.0	15 4	US-08-913-362-13 Sequence 13, Appl1
22	77.5	8.9	560 3	US-08-926-842B-13 Sequence 13, Appl1
23	77	8.9	15 4	US-08-913-362-11 Sequence 11, Appl1
24	77	8.9	15 4	US-08-913-362-13 Sequence 13, Appl1
25	75	8.6	15 4	US-08-883-515-2 Sequence 2, Appl1
26	75	8.6	15 4	US-08-913-362-18 Sequence 18, Appl1
27	75	8.6	15 4	US-08-913-362-24 Sequence 24, Appl1

28	74.5	8.6	346 2	US-08-476-254-10 Sequence 10, Appl1
29	74.5	8.6	346 6	5474933-2 Patent No. 5474933
30	74.5	8.6	346 6	5474933-7 Patent No. 5474933
31	74	8.5	264 1	US-08-482-271-3 Sequence 3, Appl1
32	74	8.5	264 2	US-08-482-271-4 Sequence 4, Appl1
33	74	8.5	264 2	US-08-854-811-45 Sequence 45, Appl1
34	74	8.5	264 3	US-09-080-120A-2 Sequence 2, Appl1
35	74	8.5	264 3	US-09-080-120A-4 Sequence 4, Appl1
36	74	8.5	264 5	PCT-US95-08925-2 Sequence 2, Appl1
37	74	8.5	264 5	PCT-US95-08925-4 Sequence 4, Appl1
38	74	8.5	291 1	US-08-468-847B-19 Sequence 19, Appl1
39	74	8.5	291 3	US-09-080-120A-7 Sequence 7, Appl1
40	74	8.5	291 5	PCT-US95-08925-7 Patent No. 5212074
41	74	8.5	291 6	US-08-476-254-2 Sequence 2, Appl1
42	74	8.5	346 2	US-08-483-101-4 Sequence 2, Appl1
43	74	8.5	866 2	US-08-286-791-2 Sequence 2, Appl1
44	73.5	8.4	1394 4	PCT-US95-10661A-2 Sequence 2, Appl1
45	73.5	8.4	1394 5	PCT-US95-10661A-2 Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-913-362-8
Sequence 8, Application US/08913362
Patent No. 6287574
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
TITLE OF INVENTION: R10UX, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-913-362-8
Query Match 100.0%; Score 870; DB 4; Length 174;

Best Local Similarity 100.0%; Pred. No. 3e-95;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSPRISAGYRINDLR 60
DB 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFTKLSIGASVITYDPTQSPVKPYFGARLSLNRAASHLGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDFTKLSIGASVITYDPTQSPVKPYFGARLSLNRAASHLGSDSF 120

QY 121 SKTSAGLVLAGSVYAVTPNVDDLADAGYRNYGVKNTVKNVRSGLSAGYRVKF 174
DB 121 SKTSAGLVLAGSVYAVTPNVDDLADAGYRNYGVKNTVKNVRSGLSAGYRVKF 174

RESULT 2
US-08-913-362-6
; Sequence 6, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-362-6

Query Match 95.9%; Score 834; DB 4; Length 174;
Best Local Similarity 95.4%; Pred. No. 5.5e-91;
Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSPRISAGYRINDLR 60
DB 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFTKLSIGASVITYDPTQSPVKPYFGARLSLNRAASHLGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDFTKLSIGASVITYDPTQSPVKPYFGARLSLNRAASHLGSDSF 120

QY 121 SKTSAGLVLAGSVYAVTPNVDDLADAGYRNYGVKNTVKNVRSGLSAGYRVKF 174
DB 121 SKTSAGLVLAGSVYAVTPNVDDLADAGYRNYGVKNTVKNVRSGLSAGYRVKF 174

RESULT 3
US-08-913-362-2
; Sequence 2, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-362-2

Query Match 94.8%; Score 825; DB 4; Length 174;
Best Local Similarity 94.3%; Pred. No. 6.4e-90;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSPRISAGYRINDLR 60
DB 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFTKLSIGASVITYDPTQSPVKPYFGARLSLNRAASHLGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDFTKLSIGASVITYDPTQSPVKPYFGARLSLNRAASHLGSDSF 120

QY 121 SKTSAGLVLAGSVYAVTPNVDDLADAGYRNYGVKNTVKNVRSGLSAGYRVKF 174
DB 121 SKTSAGLVLAGSVYAVTPNVDDLADAGYRNYGVKNTVKNVRSGLSAGYRVKF 174

RESULT 4
US-08-913-362-30
; Sequence 30, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5399
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-362-30
Query Match 94.7%; Score 823.5; DB 4; Length 175;
Best Local Similarity 94.9%; Pred. No. 9.7e-90;
Matches 166; Conservative 2; Mismatches 6; Indels 1; Gaps 1;
QY 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60
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DB 61 FAVDYTRYKKNYKAPSTDFKLYISIGASYIYDPTQSPYKPFYFARLSLNRAHHLGSSDS 119
QY 120 FSKTSAGIGVLAGSVAVTPNVLDAGYRYNYGKNTVKNVRSGLSAGYRVKF 174
DB 121 FSQTSXGIGVLAGSVAVTPNVLDAGYRYNYGKNTVKNVRSGLSAGYRVKF 175

RESULT 5
US-08-913-362-4
; Sequence 4, Application US/08913362
; Patent No. 6287574

; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5399
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-362-4
Query Match 93.5%; Score 813.5; DB 4; Length 175;
Best Local Similarity 93.7%; Pred. No. 1.5e-88;
Matches 164; Conservative 2; Mismatches 8; Indels 1; Gaps 1;
QY 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKKNYK-APSTDFKLYISIGASYIYDPTQSPYKPFYFARLSLNRAHHLGSSDS 119
DB 61 FAVDYTRYKKNYKAPSTDFKLYISIGASYIYDPTQSPYKPFYFARLSLNRAHHLGSSDS 119
QY 120 FSKTSAGIGVLAGSVAVTPNVLDAGYRYNYGKNTVKNVRSGLSAGYRVKF 174
DB 121 FSQTSXGIGVLAGSVAVTPNVLDAGYRYNYGKNTVKNVRSGLSAGYRVKF 175

RESULT 6
US-08-913-362-26
; Sequence 26, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
STRAIN: 6088
US-08-913-362-26

Query Match 15.3%; Score 133; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
DB 1 FAVDYTRYKNYKAPSTDFKLYSIGA 25

RESULT 7
US-08-127-499A-20
Sequence 20, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-20

Query Match 14.4%; Score 125; DB 1; Length 170;
Best Local Similarity 25.2%; Pred. No. 4.8e-07;
Matches 37; Conservative 18; Mismatches 46; Indels 46; Gaps 3;

QY 6 AALIALAPPAALAGCAGFYVQADAH-----AKASSLSG-----AKG 45
DB 15 SLEFSSAAQAASEDRSPYVQADLAVAEIRITHDYPQATGANNSTVSDYFNIRAH 74
QY 46 FSPRISAGYRINDLRFVADYTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGIDEGGRRIADYASIRKMNKNKSVNTKLELNKHNKKDKLTENQNGTFHA 134
QY 80 LYSIGASYIDEDTQSPYKPYFGARLS 106
DB 135 ASLGLSAYIDFKLKGKFPYIGARVA 161

RESULT 8
US-08-482-847-20
Sequence 20, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-20

Query Match 14.4%; Score 125; DB 1; Length 170;
Best Local Similarity 25.2%; Pred. No. 4.8e-07;
Matches 37; Conservative 18; Mismatches 46; Indels 46; Gaps 3;

QY 6 AALLALPAAALAGAGSGFYQADAA-----AKASSLG-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYYQADLAABRTHDPQATGANNSTVSDYFRRIRASH 74
QY 46 FSPRISAGYRINDLRFADYRKYNY-----KAPSTDFK 79
DB 75 IHPKRSVGDDEGMRILADYASIRKMNKKSVNTKELENKHNKKDKLTENQNGTFHA 134
QY 80 IYISGASVYDFDTQSPVKPYFGARLS 106
DB 135 ASSLGISAIYDFKLKGKFKPYGARVA 161

RESULT 9
US-08-457-997B-2
Sequence 2, Application US/08457997B
Patent No. 5766608

GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,997B
FILING DATE:

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gollick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-457-997B-2

Query Match 12.0%; Score 104; DB 1; Length 359;
Best Local Similarity 24.7%; Pred. No. 0.00046;
Matches 56; Conservative 29; Mismatches 82; Indels 60; Gaps 11;

QY 1 MKKALALIALALPAAALAGAGSGFYQADAA-----HAKASSLGASAGFSPRISAG 53
DB 1 MKKTAIALVAVAGLAASVAQAAPQENTFYAGYKAGQGSFHDGINNNGAIKKGLSSS-NYG 59
QY 54 YRINDLRFADVITRKNTKAPSTDFKLKLSIGASVYIDDTQSPV-----KPFAR 104

DB 60 YRRNTFTYGV-----FGYQILNOD--NFGLAELGYDDGFRAKLRGPKAKHTNNGAY 113
QY 105 LSLNRSAGAHLGSDSPSEKTSAGL-----GVLA-GVSYA 136
DB 114 LSLKGSYEVLDGIDYIGKAGVALVRSDYKFEYDANGTRDHHKGRHTARASGLFPAVGAERYA 173
QY 137 VTPNVLDAGY-----RYNYGVKNVTYKVRSS--GELSAGVRYKF 174
DB 174 VLPELAVRLEYQWLTFRGKYRPODKPWTALNYPWIGCINAGISYRF 220

RESULT 10
US-08-467-722A-2
Sequence 2, Application US/08467722A
Patent No. 6030626

GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,722A
FILING DATE:

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gollick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-722A-2

Query Match 12.0%; Score 104; DB 3; Length 359;
Best Local Similarity 24.7%; Pred. No. 0.00046;
Matches 56; Conservative 29; Mismatches 82; Indels 60; Gaps 11;

QY 1 MKKALALIALALPAAALAGAGSGFYQADAA-----HAKASSLGASAGFSPRISAG 53
DB 1 MKKTAIALVAVAGLAASVAQAAPQENTFYAGYKAGQGSFHDGINNNGAIKKGLSSS-NYG 59
QY 54 YRINDLRFADVITRKNTKAPSTDFKLKLSIGASVYIDDTQSPV-----KPFAR 104
DB 60 YRRNTFTYGV-----FGYQILNOD--NFGLAELGYDDGFRAKLRGPKAKHTNNGAY 113
QY 105 LSLNRSAGAHLGSDSPSEKTSAGL-----GVLA-GVSYA 136
DB 114 LSLKGSYEVLDGIDYIGKAGVALVRSDYKFEYDANGTRDHHKGRHTARASGLFPAVGAERYA 173
QY 137 VTPNVLDAGY-----RYNYGVKNVTYKVRSS--GELSAGVRYKF 174
DB 174 VLPELAVRLEYQWLTFRGKYRPODKPWTALNYPWIGCINAGISYRF 220

RESULT 11

Db 509 GKVASV-FDEISASKTSNAG--AGVQPNLPNPNVIDASYEYS---KIDSIK-VGTMM 561
QY 166 LSAGVR 171
Db 562 LGAGVR 567

RESULT 14

US-09-336-447A-11
; Sequence 11, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/336,447A
; CURRENT FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-11

Query Match

Best Local Similarity 26.0%; Score 83; DB 4; Length 610;
Matches 45; Conservative 21; Mismatches 55; Indels 52; Gaps 9;

QY 19 AEGASGEVYQADA-----AHAKASSSIGS-AKGFSPRISA-GYRIN--DLRFADV 65
Db 473 ASADTFKAATADAITKNGNAITKNKASTIDLTGKVDGFGRTALDTKVNADFGRITLAD 532
QY 66 TRYKN---YKAPSTDFKLYSIGASVIYDFDQSPVKPYFGARLSLNRSASHLGSDSFS 121
Db 533 SKVENGMAAQAALSGLFQPSYSGF-----NATAALGGYGSKS 570
QY 122 KTSAGLGVLAVGYAVTPVNDLDAGYRYNVGKVTNVRSGELSAQVRKF 174
Db 571 AVAIGAG-----YRVNPNLAFKAG-----AAINTSGN-KKGSYNIQVNYEF 610

RESULT 15

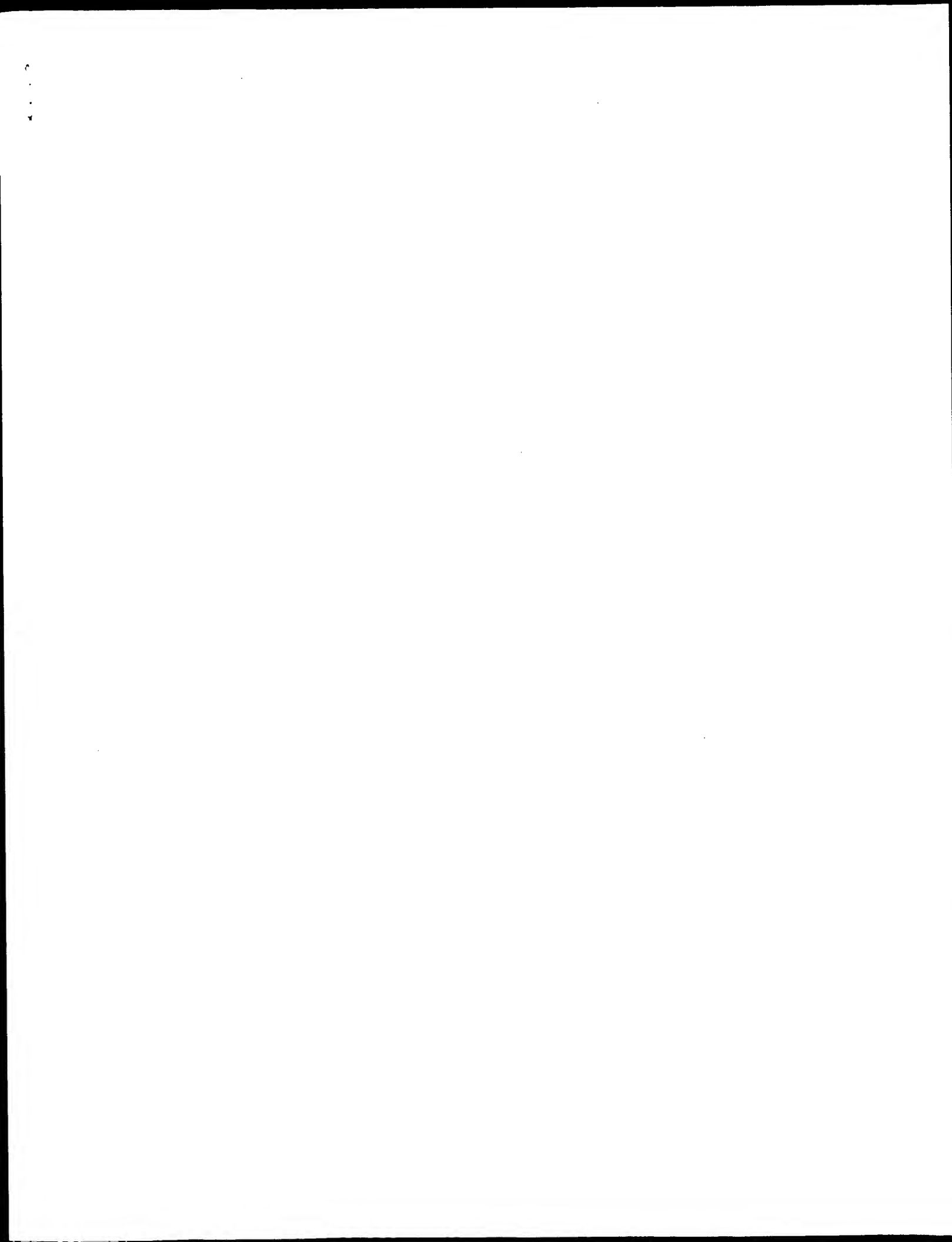
US-09-336-447A-7
; Sequence 7, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/336,447A
; CURRENT FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 624
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-7

Query Match 9.5%; Score 83; DB 4; Length 624;
Best Local Similarity 26.0%; Pred. No. 0.32;

Matches 45; Conservative 21; Mismatches 55; Indels 52; Gaps 9;

QY 19 AEGASGEVYQADA-----AHAKASSSIGS-AKGFSPRISA-GYRIN--DLRFADV 65
Db 487 ASADTFKAATADAITKNGNAITKNKASTIDLTGKVDGFGRTALDTKVNADFGRITLAD 546
QY 66 TRYKN---YKAPSTDFKLYSIGASVIYDFDQSPVKPYFGARLSLNRSASHLGSDSFS 121
Db 547 SKVENGMAAQAALSGLFQPSYSGF-----NATAALGGYGSKS 584
QY 122 KTSAGLGVLAVGYAVTPVNDLDAGYRYNVGKVTNVRSGELSAQVRKF 174
Db 585 AVAIGAG-----YRVNPNLAFKAG-----AAINTSGN-KKGSYNIQVNYEF 624

Search completed: October 28, 2002, 16:04:21
Job time : 10.4864 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:58:04 ; Search time 12.4821 Seconds

(without alignments)
1339.485 Million cell updates/sec

Title: US-09-684-883-8

Sequence: 1 MKKALALIALALPAAALAE.....VNTVKNRSGELSGAVRVKF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	834	95.9	174	2	B81932
2	829	95.3	174	2	G81174
3	237.5	27.3	261	2	S16610
4	236	27.1	270	2	S04380
5	235	27.0	260	2	S16611
6	235	27.0	266	2	S16616
7	234.5	26.9	338	2	S16612
8	234	26.8	257	2	S36343
9	233.5	26.8	257	2	S16614
10	233.5	26.8	257	2	S16614
11	233.5	26.8	257	2	S16614
12	231	26.6	258	1	KONH2C
13	231	26.6	260	1	S08514
14	231	26.6	260	1	KONH0
15	228.5	26.3	282	2	S72343
16	226	26.0	233	2	S16617
17	225.5	25.9	233	2	S36350
18	225	25.9	234	2	S36342
19	225	25.9	234	2	S36342
20	224	25.7	254	2	S20043
21	222	25.5	261	2	S16619
22	221	25.4	234	2	S36348
23	220.5	25.3	243	2	S36346
24	219	25.2	234	1	KONH8
25	219	25.2	238	2	S36349
26	216	24.8	248	2	PL0038
27	210	24.1	178	2	F64124
28	209	24.0	238	2	S36344
29	206.5	23.7	247	2	S28627

30	206	23.7	239	2	S28630	opacity protein op
31	194.5	22.4	214	2	S44706	opacity protein op
32	184.5	21.2	235	2	S44707	opacity protein op
33	176.5	20.3	121	2	I64187	opacity protein ho
34	144.5	16.6	210	2	S77737	opacity protein op
35	134	15.4	187	2	S20044	opacity protein op
36	129	14.8	239	2	S08513	opacity protein op
37	125	14.4	168	2	S08513	opacity protein op
38	125	14.4	170	2	T10256	opacity protein-re
39	124.5	14.3	281	2	AH3012	opacity protein-re
40	124.5	14.3	284	2	G98271	opacity protein-re
41	122.5	14.1	70	2	F64066	outer surface prote
42	120.5	13.9	201	2	S16286	hypothetical prote
43	120	13.8	192	2	S44712	probable outer mem
44	116.5	13.4	264	2	S44712	opacity protein op
45	114	13.1	182	2	A10353	opacity protein op
						heat resistant agg
						attachment invasio

ALIGNMENTS

RESULT 1

B81932

outer membrane protein NMA0862 [imported] - Neisseria meningitidis (strain z2491 sero

C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

C:Accession: B81932
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo

Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis z2491

A:Reference number: A81775; MUID:20222556

A:Accession: B81932

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-174 <PAR>

A:Cross-references: GB:AL162754; GB:AL157959; MID:97379424; PIDN:CAH84143.1; PID:9737

A:Experimental source: serogroup A, strain z2491

C:Genetics:

A:Gene: nspa; NMA0862

Query Match
Best local similarity 95.9%; Score 834; DB 2; Length 174;
Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAAALAEAGSGFYQADAAHAKASSISGAKGSPRSAGYRINDLR 60

Db 1 MKKALALIALALPAAALAEAGSGFYQADAAHAKASSISGAKGSPRSAGYRINDLR 60

QY 61 FADYTRKKNKAPSTDPKLYSIGASVYDFDQSPVKKPYFGARLSNRAAHILGSDSF 120

Db 61 FADYTRKKNKAPSTDPKLYSIGASVYDFDQSPVKKPYFGARLSNRAAHILGSDSF 120

QY 121 SKTSAGLGVAGVAYTPVNDIAGRYNVGVNVRNVRKVRSGELSGAVRVKF 174

Db 121 SKTSAGLGVAGVAYTPVNDIAGRYNVGVNVRNVRKVRSGELSGAVRVKF 174

RESULT 2
G81174

outer membrane protein Nsga NMB0663 [imported] - Neisseria meningitidis (strain MC58

C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

C:Accession: G81174
R:Jettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,

Hickey, E.K.; Haft, D.H.; Salberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.

Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Accession: G81174
A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-174 <PEP>
 A:Cross-references: GB:AE002420; GB:AE002098; NID:q7225876; PTDN:AAFA1081.1; PID:q722588
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:

A:Gene: NMB0663
 Query Match 95.3%; Score 829; DB 2; Length 174;
 Best Local Similarity 94.8%; Pred. No. 9, 2e-67;
 Matches 165; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

1 MKKALALALALPAALAEAGAGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 1 MKKALALALALPAALAEAGAGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALALALALPAALAEAGAGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 Oy 61 FAVDYTRYKRYKAPSTDFKLYSGASVYDFTQSPYKRYKFAKRLSLNASHLGSDSF 120
 DB 61 FAVDYTRYKRYKAPSTDFKLYSGASVYDFTQSPYKRYKFAKRLSLNASHLGSDSF 120
 Oy 121 SKTSAGVYAGVSYAVTPNVDLAGYRNYGVKNTVKNVSGELSGAVRYKF 174
 DB 121 SKTSAGVYAGVSYAVTPNVDLAGYRNYGVKNTVKNVSGELSGAVRYKF 174
 121 SQTSLGLVLTGVSIVATPNDADAGRYRNYGVKNTVKNVSGELSGAVRYKF 174

RESULT 3

Sl6610
 opacity protein opak precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
 N:Alternate names: outer membrane protein opak
 C:Species: Neisseria gonorrhoeae
 A:Variety: strain MS11
 C:Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
 C:Accession: Sl6610
 R:Bhat, K.S.; Glibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, M.L. Microbiol. 5, 1989-1991, 1991
 A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats
 A:Reference number: Sl6610; MUID:92114767
 A:Accession: Sl6610
 A:Molecule type: DNA
 A:Residues: 1-261 <BHA>
 A:Cross-references: EMBL:X52364
 A:Experimental source: strain MS11, variant 4.8
 A>Note: the authors did not translate the sequence for the signal peptide
 A>Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
 C:Genetics:

A:Gene: opak
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-261/Product: opacity protein opak #status predicted <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-75/Domain: extracellular #status predicted <EXT1>
 F:51-61/Region: semivariable region
 F:76-84/Domain: transmembrane #status predicted <TM2>
 F:89-95/Domain: transmembrane #status predicted <TM3>
 F:96-134/Domain: extracellular #status predicted <EXT2>
 F:102-129/Region: hypervariable region HV1
 F:135-149/Domain: transmembrane #status predicted <TM4>
 F:155-165/Domain: transmembrane #status predicted <TM5>
 F:166-212/Domain: extracellular #status predicted <EXT3>
 F:171-218/Region: hypervariable region HV2
 F:213-225/Domain: transmembrane #status predicted <TM6>
 F:229-237/Domain: transmembrane #status predicted <TM7>
 F:238-252/Domain: extracellular #status predicted <EXT4>
 F:253-261/Domain: transmembrane #status predicted <TM8>

Query Match 27.3%; Score 237.5; DB 2; Length 261;
 Best Local Similarity 29.3%; Pred. No. 8e-14;
 Matches 72; Conservative 22; Mismatches 61; Indels 91; Gaps 9;

Oy 15 AAALAEAG-ASGEVYQADAAHAKA-----SSLSGAKG-----FSPRI 50
 DB 21 AQAASGNGRGPYVQADALAAERITDYPPTGAKKGTITISYSDYFRNIRHSHPRV 80

Oy 51 SAGYRINDLRFAVDTRYKRYK-----KAPSTDFK-----LYS 82
 DB 81 SVGDPEFGWRIRADYATYRRKNNKYSVSIKELLRNKNRNDLKAENGTFHAYSS 140
 Oy 83 IGASVYDFTQSPYKRYKFAKRLSLNASHLGSDSF-----DSEKTS----- 124
 DB 141 LGLSAVYDFKINDKFKPKYIGARV-----AYGHVRSIDSTFKTTEVTLTGPGTTPYPR 196
 Oy 125 -----AGIGVYAGVSYAVTPNVDLAGYRNYGVKNTVKNVSGELSGAVRYKF 168
 DB 197 GKNTQMAHRESDSIRRVGLAVAGVGIDITPNTLIDGCRYHWRGLNTR-FKTHPSAL 255
 Oy 169 GVRVRF 174
 DB 256 GVRVRF 261

RESULT 4

Sl62-SF
 opacity protein P.II precursor - Neisseria gonorrhoeae (strain F62-SF and others) (fr
 C:Species: Neisseria gonorrhoeae
 A:Variety: strain F62-SF
 C:Date: 30-Jun-1991 #sequence_revision 17-Oct-1997 #text_change 13-Nov-1998
 C:Accession: S04380, Sl6504
 R:Palmer, L.; Brooks, G.F.; Falkow, S.
 Mol. Microbiol. 3, 663-671, 1989
 A:Title: Expression of gonococcal protein II in Escherichia coli by translational fus
 A:Reference number: S04380; MUID:89343653
 A:Accession: S04380
 A:Molecule type: DNA
 A:Residues: 1-270 <PAL>
 A:Cross-references: EMBL:X15780
 A:Experimental source: strain F62-SF, serogroup IB-3; clone F62-SFcl
 A>Note: the authors did not translate the sequence of the signal peptide
 A>Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
 R:Yana, M.K.; So, M.; Seifert, H.S.; Bilyard, E.; Marchal, C.
 EMBO J. 7, 4367-4378, 1988
 A:Title: Piliin expression in Neisseria gonorrhoeae is under both positive and negativ
 A:Reference number: S02017; MUID:89210824
 A:Accession: Sl6504

A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 259-270 <TAN>
 A:Cross-references: EMBL:X13965
 A:Experimental source: strain MS11A
 A>Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
 C:Genetics:

A:Gene: opak
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-270/Product: opacity protein opak #status predicted <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-75/Domain: extracellular #status predicted <EXT1>
 F:51-61/Region: semivariable region
 F:76-84/Domain: transmembrane #status predicted <TM2>
 F:89-95/Domain: transmembrane #status predicted <TM3>
 F:96-141/Domain: extracellular #status predicted <EXT2>
 F:102-136/Region: hypervariable region HV1
 F:142-156/Domain: transmembrane #status predicted <TM4>
 F:162-172/Domain: transmembrane #status predicted <TM5>
 F:173-221/Domain: extracellular #status predicted <EXT3>
 F:178-227/Region: hypervariable region HV2
 F:222-234/Domain: transmembrane #status predicted <TM6>
 F:238-246/Domain: transmembrane #status predicted <TM7>
 F:247-261/Domain: extracellular #status predicted <EXT4>
 F:262-270/Domain: transmembrane #status predicted <TM8>

Query Match 27.1%; Score 236; DB 2; Length 270;
 Best Local Similarity 27.4%; Pred. No. 1.1e-13;

Db 182 LAGGPTPTVYVPGKNTQDAHRESDSIRRVGLGAVGVIDITPMLTLDAGYRHYWGRL 241
QY 157 TVKNVRSGLSAGVRYKF 174
Db 242 NTR-FKTHEASLGAVRYRF 258

RESULT 9

S36343

Opacity protein opa57 - Neisseria gonorrhoeae (strain MS11) (fragment)
N:Alternate names: outer membrane protein opa57
C:Species: Neisseria gonorrhoeae

A:Variety: strain MS11
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999

C:Accession: S36343; S28626
R:Kupisch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
EMBO J. 12, 641-650, 1993

A:Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms of
A:Reference number: S36328; MUID:93178439

A:Accession: S36343
A:Molecule type: DNA
A:Residues: 1-237 <RUP>

A:Cross-references: EMBL:218935; NID:949331; PIDN:CAA79368.1; PID:9440797
A:Experimental source: strain MS11, variant F3

A:Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
C:Genetics:

A:Gene: opa57
C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-237/Product: opacity protein opa57 #status predicted <MAT>
F:1-19/Domain: transmembrane #status predicted <TM1>

F:20-51/Domain: extracellular #status predicted <EXT1>
F:28-37/Region: semivariable region

F:52-60/Domain: transmembrane #status predicted <TM2>
F:65-71/Domain: transmembrane #status predicted <TM3>

F:78-105/Region: hypervariable region HV1
F:111-125/Domain: transmembrane #status predicted <TM4>

F:142-188/Domain: extracellular #status predicted <EXT3>
F:147-194/Region: hypervariable region HV2

F:189-201/Domain: transmembrane #status predicted <TM6>
F:205-213/Domain: transmembrane #status predicted <TM7>

F:214-228/Domain: extracellular #status predicted <EXT4>
F:229-237/Domain: transmembrane #status predicted <TM8>

Query Match 26.8%; Score 233.5; DB 2; Length 237;
Best Local Similarity 28.9%; Pred. No. 1.6e-13;
Matches 70; Conservative 22; Mismatches 61; Indels 89; Gaps 8;

QY 17 ALAEGSGFYVQADAAH-----KASSSLGSG-----AKGFSPRISAGY 54
Db 1 ASBEGGGRGFPYQADLAAYAEHTHDYPEPTAPKNKSTVSDYFNRIRRSVHPRSVAG 60

QY 55 RINDLRFADVDTYTKYK-----KAPSTDFK-----LYSIGAS 86
Db 61 DEFGWRLADYARYRRKMNKNKYSVSIKELRNKGNRDLDAENQENCTFAVSSLSGLS 120

QY 87 VIYDPTQSPVKPYFGARLSLNRAHAHLSGS--DSFSKTS----- 124
Db 121 AYVDFLNDKFKRYIGARV---AYGHRHSIDSTFKTTEVTLLHGPTPTPTVYVPGKMT 176

QY 125 -----AGLGLVAGSYAVTPNDLDAGYRYNVGVNRYKVRSELSAGVRY 172
Db 177 QDAHRESDSIRRVGLGAVGVIDITPMLTLDAGYRHYWGRL 241

QY 173 KF 174
Db 236 RF 237

RESULT 10

S16614

Opacity protein opaF precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
C:Species: Neisseria gonorrhoeae

A:Variety: strain MS11
C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997

C:Accession: S16614
R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehmig, F.; Stern, A.; Kupsc
Mol. Microbiol. 5, 1889-1901, 1991

A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f
A:Reference number: S16610; MUID:92114767

A:Accession: S16614
A:Molecule type: DNA
A:Residues: 1-257 <BHA>

A:Cross-references: EMBL:X52368
A:Experimental source: strain MS11, variant 4.8

A:Note: The authors translated the codon ACC for residue 206 as Ala and TAT for resid
A:Note: The authors did not translate the sequence for the signal peptide

A:Note: expression of opacity proteins is regulated by the number of translated repea
of repeats place the start codon in frame with the rest of the protein

C:Genetics:
A:Gene: opaF
C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein
F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>

F:24-257/Product: opacity protein opaF #status predicted <MAT>
F:101-126/Region: hypervariable region HV1

F:132-146/Domain: transmembrane #status predicted <TM1>
F:152-162/Domain: transmembrane #status predicted <TM2>

F:163-208/Domain: extracellular #status predicted <EXT1>
F:51-60/Region: semivariable region

F:75-83/Domain: transmembrane #status predicted <TM2>
F:88-94/Domain: transmembrane #status predicted <TM3>

F:95-131/Domain: extracellular #status predicted <EXT2>
F:101-126/Region: hypervariable region HV1

F:132-146/Domain: transmembrane #status predicted <TM1>
F:152-162/Domain: transmembrane #status predicted <TM2>

F:163-208/Domain: extracellular #status predicted <EXT3>
F:168-214/Region: hypervariable region HV2

F:209-221/Domain: transmembrane #status predicted <TM6>
F:225-233/Domain: transmembrane #status predicted <TM7>

F:234-248/Domain: extracellular #status predicted <EXT4>
F:249-257/Domain: transmembrane #status predicted <TM8>

Query Match 26.8%; Score 233.5; DB 2; Length 257;
Best Local Similarity 28.8%; Pred. No. 1.8e-13;
Matches 74; Conservative 23; Mismatches 71; Indels 89; Gaps 9;

QY 2 KKALAAIALPAAALG---ASGFYVQADAAH-----KASSSLGSGK----- 44
Db 6 KKPRLFFSSSLFSSAAQAGEDGGRGFPYQADLAAYAEHTHDYPEPTGKPKKISTVSD 65

QY 45 -----GFSPRISAGYRINDLRFADVDTYTKYK-----NYKAPSTDFK----- 79
Db 66 YFRNIRTHSHPRSVSGYDFGFWRLADYARYRRKMNKNKYSVDSIKELRNKGNRDLKTE 125

QY 80 -----LYSIGASVYDPTQSPVKPYFGARLSLNRAHAHLSGS--DSFSKTS----- 124
Db 126 NOENCTFAVSSLSGLSAVYDFKLNDKFKRYIGARV---AYGHRHSIDSTFKTTEVTLLHGPTPTPTVYVPGKMT 176

QY 125 -----AGLGLVAGSYAVTPNDLDAGYRYNVGVNRYKVRSELSAGVRY 157
Db 182 SYGGLNPTVYVTEENTQNAHNSNSIRRVGLGAVGVIDITPMLTLDAGYRHYWGRL 241

QY 158 VKNVRSGLSAGVRYKF 174
Db 242 TR-FKTHEASLGAVRYRF 257

RESULT 11

KONH2C

Opacity protein P.IIC precursor - Neisseria gonorrhoeae (strain JS3) (fragments)
N:Alternate names: outer membrane protein P.IIC

C:Species: Neisseria gonorrhoeae
A:Variety: strain JS3
C:Date: 31-Mar-1992 #sequence_revision 17-Oct-1997 #text_change 08-May-1998

C:Accession: S03095; S16360
 R:van der Ley, P.
 Mol. Microbiol. 2, 797-806, 1988
 A:Title: Three copies of a single protein II-encoding sequence in the genome of *Neisseria meningitidis*.
 A:Reference number: S03095; MUID:89096501
 A:Accession: S03095
 A:Molecule type: DNA
 A:Residues: 1-268 <VAN>
 A:Cross-references: EMBL:X12625
 A:Experimental source: strain JS3
 A:Note: 241-Val was also found
 A:Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
 R:partly, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
 Infect. Immun. 55, 2026-2031, 1987
 A:Title: Antigenic and structural differences among six proteins II expressed by a single
 A:Reference number: S16360; MUID:87308643
 A:Accession: S16360
 A:Molecule type: protein
 A:Residues: 24-34 <BAR>
 C:Genetics:
 A:Gene: PiliC
 C:Superfamily: Opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-268/Product: opacity protein P.IIC #status experimental <MAT>
 F:34-42/Domain: transmembrane #status predicted <EXT1>
 F:43-74/Domain: extracellular #status predicted <EXT1>
 F:51-60/Region: semivariable region
 F:75-83/Domain: transmembrane #status predicted <TM2>
 F:88-94/Domain: transmembrane #status predicted <TM3>
 F:95-140/Domain: extracellular #status predicted <EXT2>
 F:101-135/Region: hypervariable region HV1
 F:141-155/Domain: transmembrane #status predicted <TM4>
 F:161-171/Domain: transmembrane #status predicted <TM5>
 F:172-219/Domain: extracellular #status predicted <EXT3>
 F:177-225/Region: hypervariable region HV2
 F:220-232/Domain: transmembrane #status predicted <TM6>
 F:236-244/Domain: transmembrane #status predicted <TM7>
 F:245-259/Domain: extracellular #status predicted <EXT4>
 F:260-268/Domain: transmembrane #status predicted <TM8>

Query Match 26.8%; Score 233.5; DB 1; Length 268;
 Best Local Similarity 26.5%; Pred. No. 1.9e-13;
 Matches 68; Conservative 29; Mismatches 71; Indels 89; Gaps 7;

QY 6 AALTAALPAAALAEAGSGFYVOADAHAKA-----SSSLGSAK----- 44
 DB 13 SSLFSSAARASDEGSRGPYQADLVAERITHYPRFTGKKNISTVSDYFNIRK 72
 QY 45 -GSPRIAGYRINDLRFADVITYRK-----NTRKAPS 75
 DB 73 HSHVPRVSVGDEGSRWRIADYARKMNNKYSVSIKELLRDNDSAGVRLNIQTOK 132
 QY 76 TDFK-----LSTIGASVIYDPTQSPVKPYFGARLSLRASNL----- 114
 DB 133 TEHENGTFHVAVSSIGLSTIYDPTGSRFRPYIGMRAVYGHVRHQVSVDETEIITYP 192
 QY 115 ---GGSDSEFSK-----TSAGLGVLAVGSYAVTPNVLDAGYRYNYGVKVT 157
 DB 193 SNGGKYSLSKMPKPSHHQSNIRKVGGLVINGVGFDTITPNTLDGTGRYHNMGRLEN 252

QY 158 VKNVRSGLSAGVRYK 174
 DB 253 TR-FRTHEASLGMYRF 268

RESULT 12
 S08514
 opacity protein-related protein OPM1 precursor - *Neisseria meningitidis* (strain C1938)
 N:Alternate names: outer membrane protein class 5
 C:Species: *Neisseria meningitidis*

A:Variety: strain C1938
 C:Date: 19-Mar-1997 #sequence_rev:1510n 17-Oct-1997 #text_change 20-Jun-2000
 C:Accession: S08514
 R:Stern, A.; Meyer, P.F.
 Mol. Microbiol. 1, 5-12, 1987
 A:Title: Common mechanism controlling phase and antigenic variation in pathogenic *nei*
 A:Reference number: S08513; MUID:88260884
 A:Accession: S08514
 A:Molecule type: DNA
 A:Residues: 1-258 <STP>
 A:Cross-references: EMBL:X06445; NID:g44906; PID:g1333787
 A:Experimental source: strain C1938
 A:Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
 C:Genetics:
 A:Gene: opo1
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-13,14-21/Domain: signal sequence (fragments) #status predicted <SIG>
 F:22-258/Product: opacity protein-related protein OPM1 #status predicted <MAT>
 F:33-41/Domain: transmembrane #status predicted <TM1>
 F:42-73/Domain: extracellular #status predicted <EXT1>
 F:50-59/Region: semivariable region
 F:74-82/Domain: transmembrane #status predicted <TM2>
 F:87-93/Domain: transmembrane #status predicted <TM3>
 F:94-129/Domain: extracellular #status predicted <EXT2>
 F:100-124/Region: hypervariable region HV1
 F:130-144/Domain: transmembrane #status predicted <TM4>
 F:150-160/Domain: transmembrane #status predicted <TM5>
 F:161-209/Domain: extracellular #status predicted <EXT3>
 F:166-215/Region: hypervariable region HV2
 F:210-222/Domain: transmembrane #status predicted <TM6>
 F:226-234/Domain: transmembrane #status predicted <TM7>
 F:235-249/Domain: extracellular #status predicted <EXT4>
 F:250-258/Domain: transmembrane #status predicted <TM8>

Query Match 26.6%; Score 231; DB 2; Length 258;
 Best Local Similarity 26.5%; Pred. No. 3e-13;
 Matches 70; Conservative 26; Mismatches 70; Indels 80; Gaps 7;

QY 8 LIALPAAALAEAGSGFYVOADAHAKA-----KASSISGS-----AKG 45
 DB 14 LSSAQAASDEGSRSPYQADLVAERITHYPRFTGADKOKISTVSDYFNIRAS 73
 QY 46 RSPRIAGYRINDLRFADVITYRK-----NTRKAPSTDK-----L 80
 DB 74 IHRVSVGDEGSRWRIADYARKMNNKYSVSIKELLRDNDSAGVRLNIQTOK 132
 QY 81 YSIGASVIYDPTQSPVKPYFGARLSLR-----ASAHLAGS----- 117
 DB 134 SSLGSLAIYDFKLNKPKFYIGARAVYGHVRYHNRQVSVDETEIITYP 192
 QY 118 -----DSFSKTSAGLGVLAVGSYAVTPNVLDAGYRYNYGVKVTVKNVRSGLISA 168
 DB 194 TDFKPYHSHSISLIGVINGVGFDTITPNTLDGTGRYHNMGRLENFRTHEASL 252

QY 169 GYRVK 174
 DB 253 GMYRF 268

RESULT 13
 K0NH0
 opacity protein opac precursor - *Neisseria gonorrhoeae* (strain MS11) (fragments)
 N:Alternate names: opacity protein V0; triosephosphate dehydrogenase
 C:Species: *Neisseria gonorrhoeae*
 A:Variety: strain MS11
 C:Accession: S16618; A24429; S36328; S28621
 C:Date: 31-Mar-1989 #sequence_rev:1510n 17-Oct-1997 #text_change 16-Jul-1999
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jahnig, F.; Stern, A.; Kupsc
 Mol. Microbiol. 5, 1889-1901, 1991
 A:Title: The opacity proteins of *Neisseria gonorrhoeae* strain MS11 are encoded by a f
 A:Reference number: S16610; MUID:92114767

A:Accession: S16618
 A:Molecule type: DNA
 A:Residues: 1-260 <BNA>
 A:Cross-references: EMBL:X52370
 A:Experimental source: strain MS11, variant 4.8
 A>Note: the authors translated the codon CCA for residue 32 as Thr
 A>Note: the authors did not translate the sequence for the signal peptide
 A>Note: expression of opacity proteins is regulated by the number of translated repeat
 of repeats place the start codon in frame with the rest of the protein
 R:Stern, A.; Brown, M.; Nickel, P.; Meyer, T.F.
 Cell 47, 61-71, 1986
 A>Title: Opacity genes in *Neisseria gonorrhoeae*: control of phase and antigenic variation
 A:Reference number: A90887; MUID:87002493
 A:Accession: A24439
 A:Molecule type: DNA
 A:Residues: 25-260 <STE>
 A>Note: this protein is synthesized as a precursor; however, the authors are uncertain
 of the exact position of the start codon
 R:Kusich, E.M.; Krepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
 EMBO J. 12, 641-650, 1993
 A>Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms of
Neisseria gonorrhoeae
 A:Reference number: S36328; MUID:93178439
 A:Accession: S36328
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 25-260 <KUP>
 A:Cross-references: EMBL:Z18927; NID:949323; PIDN:CAA79360.1; PID:940789
 R:Meyer, T.F.
 submitted to the EMBL Data Library, November 1992
 A:Reference number: S28617
 A:Accession: S28617
 A:Molecule type: DNA
 A:Residues: 25-260 <MEY>
 A:Cross-references: EMBL:Z18927; NID:949323; PIDN:CAA79360.1; PID:940789
 C:Genetics:
 A:Gene: opaC
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-11,12-24/Domain: signal sequence (fragments) #status predicted <SIG>
 F:25-260/Product: opacity protein opaC #status predicted <MAT>
 F:35-43/Domain: transmembrane #status predicted <TM1>
 F:44-75/Domain: extracellular #status predicted <EXT1>
 F:52-61/Region: semivariable region
 F:76-84/Domain: transmembrane #status predicted <TM2>
 F:89-95/Domain: transmembrane #status predicted <TM3>
 F:96-134/Domain: extracellular #status predicted <EXT2>
 F:102-129/Region: hypervariable region HV1
 F:135-149/Domain: transmembrane #status predicted <TM4>
 F:155-165/Domain: transmembrane #status predicted <TM5>
 F:166-211/Domain: extracellular #status predicted <EXT3>
 F:171-217/Region: hypervariable region HV2
 F:212-224/Domain: transmembrane #status predicted <TM6>
 F:228-236/Domain: transmembrane #status predicted <TM7>
 F:237-251/Domain: extracellular #status predicted <EXT4>
 F:252-260/Domain: transmembrane #status predicted <TM8>

Query Match 26.6%; Score 231; DB 1; Length 260;
 Best Local Similarity 27.9%; Pred. No. 3e-13;
 Matches 70; Conservative 25; Mismatches 70; Indels 86; Gaps 7;

QY 6 AALIALPALAEGASCFYQADAAHA-----KASSLSGASAGFS----- 47
 DB 14 SLLFSSAQAQASEDEGRPYQADLAAYEHITHDYPRPTDSKSKISTVSDFYNINFT 73
 QY 48 ----PRISAGYRINDREFADVTRY-----KTKKASTD-- 77
 DB 74 HSTHPRVSVGYDEGGRRIADARYARKMSDNKYSVSKMRYVHKHNSNRKMLKTENOENG 133
 QY 78 --FKLYSIGASYIDPDTQSVPKPYFGARLS----- 106
 DB 134 SFHNVSSLSGLSALYDFQINDKFPYIGARVAGVHSHSDTKTKITGLTTSTPGMSGV 193
 QY 107 ---LNASAHILGSDSFSKTSAGLGLVAGVSTAVTPNDLDAGRYRYVGVKVVYKNNVS 163

DB 194 YKVARTPGAH---RESNSTRVGLVAGVGFTTPKLTLDAGRYVHNMGRLENTF-FRT 249
 QY 164 GEISAGVRYKF 174
 DB 250 HEASLGVRYRF 260

RESULT 14
 S72343
 Opacity protein opaH precursor - *Neisseria gonorrhoeae* (isolate 15063G)
 N:Alternate names: cell invasion protein opaH
 C:Species: *Neisseria gonorrhoeae*
 A:Variety: isolate 15063G
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
 C:Accession: S72343
 R:Waldeser, L.S.; Ajloka, R.S.; Metz, A.U.; Puaol, D.; Lhn, L.; Thomas, M.; So, M.
 Mol. Microbiol. 13, 919-928, 1994
 A>Title: The opaH locus of *Neisseria gonorrhoeae* MS11A is involved in epithelial cell
 A:Reference number: S72343; MUID:95115561
 A:Accession: S72343
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-283 <MAL>
 A:Cross-references: EMBL:U13708; NID:9535357; PIDN:AA474082.1; PID:9535358
 A:Experimental source: isolate 15063G
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
 A>Note: expression of opacity proteins is regulated by the number of translated repeat
 of repeats place the start codon in frame with the rest of the protein
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-48/Domain: signal sequence #status predicted <SIG>
 F:49-283/Product: opacity protein opaH #status predicted <MAT>
 F:58-66/Domain: transmembrane #status predicted <TM1>
 F:67-98/Domain: extracellular #status predicted <EXT1>
 F:75-84/Region: semivariable region
 F:99-107/Domain: transmembrane #status predicted <TM2>
 F:112-118/Domain: transmembrane #status predicted <TM3>
 F:119-155/Domain: extracellular #status predicted <EXT2>
 F:125-150/Region: hypervariable region HV1
 F:156-170/Domain: transmembrane #status predicted <TM4>
 F:176-186/Domain: transmembrane #status predicted <TM5>
 F:187-234/Domain: extracellular #status predicted <EXT3>
 F:192-240/Region: hypervariable region HV2
 F:235-247/Domain: transmembrane #status predicted <TM6>
 F:251-259/Domain: transmembrane #status predicted <TM7>
 F:260-274/Domain: extracellular #status predicted <EXT4>
 F:275-283/Domain: transmembrane #status predicted <TM8>

Query Match 26.6%; Score 231; DB 2; Length 283;
 Best Local Similarity 28.2%; Pred. No. 3.3e-13;
 Matches 70; Conservative 25; Mismatches 65; Indels 88; Gaps 8;

QY 10 AALPALAELASGCFYQADAAHA-----SSLSGASAG-----FS 47
 DB 41 SLLAQAQASEEMRPGPYQADLAERITHDYDEPTGCTISTVSDFYRNIRTHSVH 100
 QY 48 PRISAGYRINDREFADVTRYKNT-----KAPS-----TDRKLY 81
 DB 101 PRVSVGYDEGGRRIADARYARKNNNNKYSVNIERYQEAHSHNRIDLAENENGTFAVS 160
 QY 82 SIGASVYIDPDTQSVPKPYFGARLSLNASAHLGGS--DSFSKTS----- 124
 DB 161 SLGSAVYDFKLNDFKPYIGARV---AYGHVHSHSDTKTKITLISFYGVATKPTTY 216
 QY 125 -----AGLGLVAGVSTAVTPNDLDAGRYRYVGVKVVYKNNVS 166
 DB 217 DIGPKTQAHQESNIRVAGLGVAGVGFTTPKLTLDGRYVHNMGRLENTF-FKTHFA 275
 QY 167 SAGVRYKF 174
 DB 276 SLGMRYRF 283

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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:55:44 ; Search time 6.98996 Seconds

(without alignments)
963.840 Million cell updates/sec

Title: US-09-684-883-8

Perfect score: 870
Sequence: 1 MKKALALALALPAALAE.....VNTVKNVSGELSGVRVK 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	233.5	26.8	237	1	OPAK_NEIGO
2	233.5	26.8	270	1	OPAK_NEIGO
3	232	26.7	260	1	OPAL_NEIGO
4	226	26.0	233	1	OPAB_NEIGO
5	225.5	25.9	234	1	OPAB_NEIGO
6	225.5	25.9	237	1	OPAB_NEIGO
7	225	25.9	234	1	OPAF_NEIGO
8	225	25.9	236	1	OPAF_NEIGO
9	225	25.9	236	1	OPAF_NEIGO
10	222	25.5	238	1	OPAF_NEIGO
11	221	25.4	234	1	OPAF_NEIGO
12	220.5	25.3	243	1	OPAD_NEIGO
13	220	25.3	244	1	OPAD_NEIGO
14	219	25.2	234	1	OPAD_NEIGO
15	219	25.2	234	1	OPAD_NEIGO
16	210	24.1	178	1	YES7_HAEIN
17	209	24.0	238	1	OP68_NEIGO
18	206.5	23.7	247	1	OPAG_NEIGO
19	206	23.7	239	1	OPAG_NEIGO
20	176.5	20.3	121	1	OPRA_HAEIN
21	125	14.4	170	1	OPR3_NEIGO
22	122.5	14.1	70	1	Y414_HAEIN
23	115	13.2	182	1	ATL_YERPS
24	107	12.3	353	1	OM52_HAEIN
25	106	12.2	353	1	OM51_HAEIN
26	104	12.0	359	1	OM53_HAEIN
27	101	11.6	213	1	OM25_BRUVA
28	98.5	11.3	341	1	OMPU_VIBCH
29	98	11.0	349	1	OMPA_BUCAI
30	95.5	10.7	212	1	OMPA_ECOLI
31	93.5	10.7	350	1	OMPA_SALTY
32	93	10.7	213	1	OM25_BRUSU
33	93	10.7	521	1	TSAS_RICHS

34	91	10.5	213	1	OM25_BRUME	045321 bruceia me
35	87.5	10.1	240	1	OM31_BRUME	045322 bruceia me
36	87	10.0	178	1	ATL_YEREN	P16454 yerstina en
37	87	10.0	201	1	OM25_BRUCV	045335 bruceia ov
38	87	10.0	213	1	OM25_BRUCA	045110 bruceia ca
39	86.5	9.9	346	1	OMPA_ECOLI	P02934 escherichia
40	86.5	9.9	428	1	OM47_PASMU	P06003 pasteurella
41	85	9.8	213	1	OM25_BRUME	045326 bruceia ne
42	85	9.8	351	1	OM32_COMAC	P24305 comamonas a
43	84	9.7	172	1	OMPX_ENTCL	P25253 enterobacte
44	81.5	9.4	995	1	Y109_YEAST	P40442 saccharomyc
45	81	9.3	350	1	FORF_PSEAE	P13794 pseudomonas

ALIGNMENTS

RESULT 1	OPAK_NEIGO	STANDARD;	PRT;	237 AA.
ID	OPAK_NEIGO			
AC	004880;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 32, Last sequence update)			
DT	01-NOV-1995 (Rel. 32, Last annotation update)			
DE	Opacity protein OPA57 precursor (Fragment).			
GN	OPAK.			
OS	Neisseria gonorrhoeae.			
CC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=485;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MS11 / F3;			
RA	MEDLINE=93178439; PubMed=8440254;			
RX	Kusch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;			
RT	"Variable opacity (Opa) outer membrane proteins account for the cell			
RT	tropisms displayed by Neisseria gonorrhoeae for human leukocytes and			
RT	epithelial cells."			
RL	EMBO J. 12:641-650(1993).			
CC	-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA			
CC	PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE			
CC	VARIATION.			
CC	-1- SUBCELLULAR LOCATION: Outer membrane.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; Z18935; CAA79368.1; -			
DR	PIR; S28626; S28626.			
DR	InterPro: IPR003394; Opacity.			
DR	Pfam: PF02462; Opacity; 1.			
KW	Outer membrane; Multigene family; Signal.			
FT	NON_TER 1			
FT	SIGNAL <1			
FT	CHAIN 2			
FT	NON_TER 237			
SO	SEQUENCE 237 AA; 26703 MW; F8B1A07B5C7EBCAD CRC64;			
Query Match	26.8%; Score 233.5; DB 1; Length 237;			
Best Local Similarity	28.9%; Pred. No. 3e-14;			
Matches	70; Conservative 22; Mismatches 61; Indels 89; Gaps 8;			
DB	17 ALAAGAGFVQDAARA-----KASSLSGS-----AKGSPRISAGY 54			
DB	1 ASDEGGGPTVQDLATAYEHITHDPEPTAPKNKISTVSDYFRNIRRSVHPVSVGY 60			
DB	55 RINDLRFAVYVTRYKNY-----KAPSTDFK-----LYSIGAS 86			
DB	61 DFGWMRIADYARYRRKNNKNNKYSVSIKELLRNKGNGNRDLDKAEQNDNGTFHAAVSLGS 120			

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QY 87 VIVDFDTQSPVRYKPGARLSINRASHLGG--DSFSEKTS----- 124
Db 121 AYVDFKLNDEKFKPYIGARV---AYGHVRSIDSTIKTTEVTTLHGPGTTPPYVPGKNT 176
QY 125 -----AGLGVLAGVSYAVTPNVVDLDAGYRNTYGVKYNVKNVSGELSGAGVRY 172
Db 177 QDAHRESDSIRRYGLGAVAGVGIDITPNTLDAGYRHYWGRLENNR-FKTHBASLGAVRY 235
QY 173 KF 174
Db 236 RF 237

RESULT 2
OMPC_NEIGO STANDARD; PRT; 270 AA.
ID OMPC_NEIGO
AC P09888;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Outer membrane protein P.IIC precursor (Protein IIC).
GN P.IIC.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J53;
RX MEDLINE=89096501; PubMed=3145386;
RA van der Ley P.;
RT "Three copies of a single protein II-encoding sequence in the genome
RT of Neisseria gonorrhoeae J53: evidence for gene conversion and gene
RT duplication."
RL Mol. Microbiol. 2:797-806(1988).
CC -I- FUNCTION: THIS PROTEIN SERVES AS A PORIN.
CC -I- SUBUNIT: HOMOTRIMER.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC CC
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CC -----
CC EMBL: X12625; CAA31144.1;
CC PIR: S03095; KONHZC.
CC DR InterPro: IPR003394; Opacity: 1.
CC DR Pfam: PF02462; Opacity: 1.
CC KW Outer membrane; Porin; Transmembrane; Antigen; Signal.
CC FT SIGNAL 1 25
CC FT CHAIN 26 270 OUTER MEMBRANE PROTEIN P.IIC.
CC FT TRANSMEM 36 44 POTENTIAL.
CC FT TRANSMEM 77 85 POTENTIAL.
CC FT TRANSMEM 90 96 POTENTIAL.
CC FT TRANSMEM 143 157 POTENTIAL.
CC FT TRANSMEM 163 173 POTENTIAL.
CC FT TRANSMEM 222 234 POTENTIAL.
CC FT TRANSMEM 238 246 POTENTIAL.
CC FT TRANSMEM 262 270 POTENTIAL.
CC SQ SEQUENCE 270 AA; 30269 MW; F6B448373830A50D CRC64;

Query Match 26.8%; Score 233.5; DB 1; Length 270;
Best Local Similarity 26.5%; Pred. No. 3.4e-14;
Matches 66; Conservative 29; Mismatches 71; Indels 89; Gaps 7;
QY 6 AATIALALPAALALAGASGVYQADAHAHA-----SSSIGSAK----- 44
Db 15 SSLFSSAARAAASDGGGPGYQADLAVAAERITHDPKPTGCKNKISTVSDYFRNIRT 74
QY 45 -GSPRISAGYRINDLPAVDYTRYK-----NYKAPS 75

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Db 75 HSHVPRVSYGDFGSMRIADYARYRKNNKYSVSIKELLRDNDSASVGHILNIQTK 134
QY 76 TDFK-----LYSIGAVTYDEFTQSPVRYKPGARLSINRASHL----- 114
Db 135 TEHENGTEFHAVSSIGLSTIYDFDTGSEFRPYIGMRAVYGHVRHQVSVBOEFTIITYP 194
QY 115 ---GGSDFSK-----TSAGLGVLAGVSYAVTPNVVDLDAGYRNTYGVKYNVKNVSGELSGAGVRY 157
Db 195 SNGGKYSVLSKMPKSAHHOSNSIRRYGLGVINGVGFDTITPNTLDGYRYHNMGRLEN 254
QY 158 VKNVSGELSGAGVRYKE 174
Db 255 TR-FKTHBASLGMYRYF 270

RESULT 3
OPRI_NEIMC STANDARD; PRT; 260 AA.
ID OPRI_NEIMC
AC P10170;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Opacity-related protein POPM1.
GN Opr.
OS Neisseria meningitidis (serogroup C).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=135720;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1938 / SEROGROUP C;
RX MEDLINE=88260884; PubMed=2455211;
RA Stern A., Meyer T.F.;
RT "Common mechanism controlling phase and antigenic variation in
RT pathogenic neisseriae."
RL Mol. Microbiol. 1:5-12(1987).
CC -I- SUBCELLULAR LOCATION: Outer membrane.
CC -I- SIMILARITY: STRONG TO THE OPACITY-RELATED PROTEIN POPM3 AND
CC REGIONS OF HOMOLOGY WITH N.GONORRHOEA (STRAIN MS11) OPA GENE
CC PRODUCTS.
CC CC
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CC -----
CC EMBL: X06445; CAA29748.1; ALT_SEQ.
CC PIR: S08514; S08514.
CC DR InterPro: IPR003394; Opacity: 1.
CC DR Pfam: PF02462; Opacity: 1.
CC KW Outer membrane.
CC SQ SEQUENCE 260 AA; 28936 MW; EB47A2843B3F037B CRC64;

Query Match 26.7%; Score 232; DB 1; Length 260;
Best Local Similarity 27.6%; Pred. No. 4.5e-14;
Matches 71; Conservative 31; Mismatches 69; Indels 86; Gaps 8;
QY 3 KALAAIALALPAALALAGASGVYQADAHAHA-----KASSSIG 41
Db 5 KTFSSLLFSSLLFSSAAQAASDGSRSPPYQADLAVAAERITHYPPPTGADDKSTIV 64
QY 42 S-----AKGSPRISAGYRINDLPAVDYTRYK-----NYKAPST 76
Db 65 SDYFRIRARHSHPRKVSQYDGGRIADYASYSKKMESNSTKYTEIKDKNTKEKT 124
QY 77 DFK-----LYSIGAVTYDEFTQSPVRYKPGARLSINR-----ASGHL 114
Db 125 EHQQNGSFHATSSLGSAIYDEKLNDEKFKPYIGAVVAAGHVKHQVSEYETKTTVTSKPK 184
QY 115 GGS-----DSFSEKTSAGLGVLAGVSYAVTPNVVDLDAGYRNTYGVKYNV 157

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Db 185 GGTAGAGVATKTPDPPYHSHSISLGLGAGVGFDTPLKLTDTGYRHNWGLLEN 244
 QY 158 VKNVRSGLSAGVRKF 174
 Db 245 TR-FKTHASLGVRKF 260

RESULT 4

OP67_NEIGO
 ID OP67_NEIGO STANDARD: PRT: 233 AA.
 AC 005034;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA67 precursor (Fragment).
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VPI;
 RA MEDLINE=93178439; PubMed=8440254;
 RT Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 RT epithelial cells."
 RL EMBO J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
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 CC
 DR EMBL: Z18942; CAA79375.1;
 DR PIR: S28625; S28625.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1
 FT CHAIN 2 >233 POTENTIAL.
 FT NON_TER 233 OPACITY PROTEIN OPA67.
 SQ SEQUENCE 233 AA; 26039 MW; 6C13AA6AB163C67F CRC64;

Query Match 26.0%; Score 226; DB 1; Length 233;
 Best Local Similarity 27.8%; Pred. No. 1.4e-13;
 Matches 66; Conservative 27; Mismatches 58; Indels 86; Gaps 8;

QY 19 AEG-ASGFYVQADAHA-----KASSISGSAKF-----SPRISAGY 54
 Db 2 SEGNGRGYVQADLAAYEAHITHDYPQGTGKKNKISTVSDYFNINRTHSHRVSAGYD 61
 QY 55 RINDLRANDYTRYK--NYKASTDFK-----LYSIGASVY 89
 Db 62 DFGWMLADYARVYKMDNKSVDIKELKNKONKRDJKTENQENGTFHVVSLGASVY 121
 QY 93 TQSPVAPYFGARLSLNRASAHLGGS-DSFSTK-----LVSIGASVY 174
 Db 122 LMDKRPYIGARV-----AYGVRHSIDSTYKTTGFLTAGARGAAPVSSPYKNTQDAHQ 177
 QY 125 -----AGLGLAGVSYAVTPNVLDAGYRYNYGVKNTVKNVRSGLSAGVRKF 174
 Db 178 ESNISIRVGLGAGVGFDTPLKLTDTGYRHNWGLLENR-FKTHASLGVRKF 233

RESULT 5

OPAB_NEIGO
 ID OPAB_NEIGO STANDARD: PRT: 234 AA.
 AC 004874;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA51 precursor (Fragment).
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RA MEDLINE=93178439; PubMed=8440254;
 RT Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 RT epithelial cells."
 RL EMBO J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
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 CC
 DR EMBL: Z18928; CAA79361.1;
 DR PIR: S28628; S28628.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1
 FT CHAIN 2 >234 POTENTIAL.
 FT NON_TER 234 OPACITY PROTEIN OPA51.
 SQ SEQUENCE 234 AA; 26772 MW; 9FE5B5DABBA96CA CRC64;

Query Match 25.9%; Score 225.5; DB 1; Length 234;
 Best Local Similarity 29.0%; Pred. No. 1.0e-13;
 Matches 69; Conservative 22; Mismatches 60; Indels 87; Gaps 9;

QY 19 AEG-ASGFYVQADAHA-----KASSISGSAK-----GFSPRISAGY 55
 Db 2 SEGNGRGYVQADLAAYEAHITHDYPQGTGKKNKISTVSDYFNINRTHSHRVSAGYD 61
 QY 56 INDLRANVYTRYK--NYKASTDFK-----LYSIGASVY 89
 Db 62 DFGWMLADYARVYKMDNKSVDIKELKNKONKRDJKTENQENGTFHVVSLGASVY 121
 QY 90 DEDTQSPVAPYFGARLSLNRASAHLGGS-DSFSTK-----LVSIGASVY 174
 Db 122 DFKLNGKFPYIGARV-----AYGVRHSIDSTYKTTGFLTAGARGAAPVSSPYKNTQDAHQ 177
 QY 125 -----AGLGLAGVSYAVTPNVLDAGYRYNYGVKNTVKNVRSGLSAGVRKF 174
 Db 178 HOSNISIRVGLGAGVGFDTPLKLTDTGYRHNWGLLENR-FKTHASLGVRKF 234

RESULT 6

OPAB_NEIGO
 ID OPAB_NEIGO STANDARD: PRT: 237 AA.
 AC 004882;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA58 precursor (Fragment).
 GN OPA58
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 epithelial cells."
 RT EMBO J. 12:641-650(1993).
 RL EMBO J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
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 CC -----
 CC EMBL: Z18937; CAA79370.1; -
 DR PIR: S28624; S28624.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >237 OPACITY PROTEIN OPA58.
 FT NON_TER 237 237
 FT SEQUENCE 237 AA; 26855 MW; B165033B2CDB6A53 CRC64;
 SQ
 Query Match 25.9%; Score 225.5; DB 1; Length 237;
 Best Local Similarity 28.9%; Pred. No. 1.6e-13;
 Matches 68; Conservative 21; Mismatches 57; Indels 89; Gaps 8;
 QY 24 GYVQADAAHA-----KASSSLGSAK-----PRISAGYRINDLRF 61
 DB 8 GYVQADLAAYEHITHDYPEQTPGKISTVSDYFRNIRTHSHIPRVSVGYDFGGMRI 67
 QY 62 AVDYTRYK-----KAPSTDFK-----LYSGASVIYDFDT 93
 DB 68 AADYARRKWNNKYSVSIKELLNKNGMKTENQENGTFHVAVSSGLSAVDKFL 127
 QY 94 QSPKPFGARLSNRSASHLGGS-DSFSKTS-----LXSGASVIYDFDT 124
 DB 128 NDKRPYIGARV-----AYGVRHSIDSTKTKTETITLLHGPCTTPYVPEKNTQDAHRES 183
 QY 125 -----AGLGVLAGVSYAVTPNDLDAGRYNYGKVNFKVNSGELSGAVRYKF 174
 DB 184 DSIRRVGAGVAGVGDITPMLTLDAGRYHYWGLNTR-FKTHASLGYRYKF 237
 RESULT 7
 OPAE_NEIGO STANDARD; PRT; 234 AA.
 ID OPAE_NEIGO
 AC 004878;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA55 precursor (Fragment).
 GN OPAE.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 epithelial cells."
 RT EMBO J. 12:641-650(1993).
 RL EMBO J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
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 CC -----
 CC EMBL: Z18933; CAA79366.1; -
 DR PIR: S28632; S28632.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >234 OPACITY PROTEIN OPA55.
 FT NON_TER 234 234
 FT SEQUENCE 234 AA; 26681 MW; BEB30B3A774C766 CRC64;
 SQ
 Query Match 25.9%; Score 225; DB 1; Length 234;
 Best Local Similarity 28.9%; Pred. No. 1.7e-13;
 Matches 67; Conservative 21; Mismatches 58; Indels 86; Gaps 8;
 QY 24 GYVQADAAHA-----KASSSLGSAK-----GFSPRISAGYRINDLRF 61
 DB 8 GYVQADLAAYEHITHDYPEQTPGKISTVSDYFRNIRTHSHIPRVSVGYDFGGMRI 67
 QY 62 AVDYTRYK-----KAPSTDFK-----LYSGASVIYDFDT 95
 DB 68 AADYARRKWNNKYSVSIKELLNKNGMKTENQENGTFHVAVSSGLSAVDKFL 127
 QY 96 PVKPFGARLSNRSASHLGGS-DSFSKTS-----LXSGASVIYDFDT 124
 DB 128 KRPYIGARV-----AYGVRHSIDSTKTKTETITLLHGPCTTPYVPEKNTQDAHRES 183
 QY 125 -----AGLGVLAGVSYAVTPNDLDAGRYNYGKVNFKVNSGELSGAVRYKF 174
 DB 184 RNVGLGVLAGVGFDTPKLLDTGYRYHWGLNTR-FKTHASLGYRYKF 234
 RESULT 8
 OPAE_NEIGO STANDARD; PRT; 234 AA.
 ID OPAE_NEIGO
 AC 004879;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA56 precursor (Fragment).
 GN OPAE.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 epithelial cells."
 RT EMBO J. 12:641-650(1993).
 RL EMBO J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
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 CC -----
 CC EMBL: Z18933; CAA79366.1; -
 DR PIR: S28632; S28632.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >234 OPACITY PROTEIN OPA55.
 FT NON_TER 234 234
 FT SEQUENCE 234 AA; 26681 MW; BEB30B3A774C766 CRC64;
 SQ

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RL EMBL J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
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CC -----
DR EMBL; Z18934; CAA79367.1; -.
DR PIR; S28620; S28620.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
DR Outer membrane; Multigene family; Signal.
FT SIGNAL 1 1
FT NON_TER 1 1
FT CHAIN 2 >234 POTENTIAL.
FT NON_TER 2 234 OPACITY PROTEIN OPA56.
SQ SEQUENCE 234 AA; 26868 MW; 5175C6606839EFB CRC64;

Query Match 25.9%; Score 225; DB 1; Length 234;
Best Local Similarity 28.4%; Pred. No. 1.7e-13;
Matches 66; Conservative 22; Mismatches 58; Indels 86; Gaps 8;

QY 24 GFVYQADAAHA-----KASSSLGSAK-----GFSPRISAGYRINDLR 61
DB 8 GFVYQADAAVAEHTHDYDEQGTGKKDKISTVSDYFRNKRTHSIHPRYSVGDDEGMRI 67
QY 62 AVDTYRKNTKAP--STDFK-----LYSIGASYVDPTOS 95
DB 68 AADYARIRKNDKYSYDIKELENKQNKRDLEKQENGTFFHAYSSLSGASVYDKLMD 127
QY 96 PVKPYFGARSLNRASHGGS--DSFSKTS----- 124
DB 128 KFPYIGARV---AYGHVHSHIDSTKTKTKFTLTSSYGGINPTVTEONTNANHOSNSI 183
QY 125 --AGLVLGASVYAVTPNDLDAGYRNYGKNTVKNVRSGLSAGVYKF 174
DB 184 RRVGLGVIAGVGFDITPKLITLDGGRYHMGRLNTR-EKTHPASLGAVYRF 234

RESULT 9
OPAC_NEIGO STANDARD; PRT; 236 AA.
ID OPAC_NEIGO P11296;
AC P11296;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA50 precursor (OPA50) (V0) (Fragment).
GN OPAC.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=MS11 / V0;
RX MEDLINE=87002493; PubMed=3093085;
RA Stern A., Brown M., Nickel P., Meyer T.F.;
RT "Opacity genes in Neisseria gonorrhoeae: control of phase and
RT antigenic variation.";
RL Cell 47:61-71(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kusch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and

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RT epithelial cells.";
RL EMBL J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
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CC -----
DR EMBL; M14746; -; NOT_ANNOTATED_CDS.
DR PIR; A24429; KONHO.
DR PIR; S28621; S28621.
DR PIR; S36328; S36328.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
DR Outer membrane; Multigene family; Signal.
FT SIGNAL 1 1
FT NON_TER 1 1
FT CHAIN 2 >236 POTENTIAL.
FT NON_TER 2 236 OPACITY PROTEIN OPA50.
SQ SEQUENCE 236 AA; 26685 MW; 68DC237692183398 CRC64;

Query Match 25.9%; Score 225; DB 1; Length 236;
Best Local Similarity 28.3%; Pred. No. 1.7e-13;
Matches 68; Conservative 21; Mismatches 65; Indels 86; Gaps 7;

QY 17 ALAEGASGFYQADAAHA-----KASSSLGSAKGS-----PRISAGY 54
DB 1 ASEDGGRGYPQADAAVAEHTHDYPRKTPDSKGIISTVSDYFRNKRTHSIHPRYSVGD 60
QY 55 RINDRFAVDYTRY-----KNKAPSTD-----FKLISGAS 86
DB 61 DCGGRIRIADARVARKKMSDNKYSIKMKRVRKHNKRNKLNKTEQENGSPHAYSSLS 120
QY 87 VYDFDTSVPKPYFGARLS-----LNRSASHL 114
DB 121 AIDYFOINDKRPYIGARVAGVHSHIDSTKTKITGLTSTPGIMSGYVVLTPPAH- 179
QY 115 GGSDFSEKTSAGLGVAVTPNDLDAGYRNYGKNTVKNVRSGLSAGVYKF 174
DB 180 --RESDSIRRVGLGVIAGVGFDITPKLITLDGGRYHMGRLNTR-EKTHPASLGAVYRF 236

RESULT 10
OPAH_NEIGO STANDARD; PRT; 238 AA.
ID OPAH_NEIGO 004884;
AC 004884;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Opacity protein OPA60 precursor (Fragment).
GN OPAH.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kusch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RL EMBL J. 12:641-650(1993).
RN [2]
RP SEQUENCE FROM N.A.

```

RC STRAIN-MS11 / V18;
 RX MEDLINE=92114767; PubMed=1815562;
 RA Bat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnis F.,
 RA Stern A., Kupsch E.-M., Meyer T.F., Swanson J.;
 RT "The opacity proteins of *Neisseria gonorrhoeae* strain MS11 are
 RT encoded by a family of 11 complete genes.";
 RL Mol. Microbiol. 5:1889-1901(1991).
 RN [1].
 RP ERRATUM.
 RA MEDLINE=92261333; PubMed=1584024;
 RA Bat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnis F.,
 RA Stern S., Kupsch E.-M., Meyer T.F., Swanson J.;
 RL Mol. Microbiol. 6:1073-1076(1992).
 CC -1- FUNCTION: ARE IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Z18939; CAA79372.1; -;
 DR EMBL: X60711; CAA43121.1; -;
 DR PIR: S28631; S28631.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >238 OPACITY PROTEIN OPA60.
 FT VARIANT 2 234 SED -> MLKA (IN MS11 / V18).
 FT VARIANT 234 234 V -> M (IN MS11 / V18).
 FT NON_TER 238
 SQ SEQUENCE 238 AA; 27073 MW; 883A3560C2DF1B9F CRC64;
 Query Match 25.5%; Score 222; DB 1; Length 238;
 Best Local Similarity 28.0%; Pred. No. 3.3e-13;
 Matches 68; Conservative 22; Mismatches 63; Indels 90; Gaps 7;
 QY 17 ALAEGASGVYQADAAHA-----KASSSLGS-----AKGSEPRISAGY 54
 DB 1 ASEGGRRPPYQADLAAYEHITHDYPEPTAPKPKNSTVSDYFRNIRTRSVHPRVSGY 60
 QY 55 RINDLRFAVDYTRYKN-----KAPSTDFKLYSTGAS 86
 DB 61 DFGGRRIRADARFRKNNNNRYSVNIENVRIRKNGIRIDRKTENQNGTFHVAVSLGLS 120
 QY 87 VIYDFDTQSPKPYFGARLSLRASAHLGGS-DSFSKT-----123
 DB 121 AIYDFQIDKRPYIGARV-----AYGVRHSIDSTKTIETVTPSPNAPCAVTTYWDP 176
 QY 124 -----SAGLVLAGVSYAVTPNVDLAGYRNYGVKNTYKNNVSGELSGAVR 171
 DB 177 KTQNDYQNSIRVGLGIYAGVGDITPKLTLDAGYRHYHNGRLENTR-FKTHASISGLVR 235
 QY 172 VKF 174
 DB 236 YRF 238
 RESULT 11
 ID OP65_NEIGO STANDARD; PRT; 234 AA.
 AC 004885;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA65 precursor (Fragment).

OS *Neisseria gonorrhoeae*.
 CC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 CC NCBL_TaxID=485;
 RX SEQUENCE FROM N.A.
 RP STRAIN-VPI;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 RT tropisms displayed by *Neisseria gonorrhoeae* for human leukocytes and
 RT epithelial cells";
 RL EMBD J.12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Z18940; CAA79373.1; -;
 DR PIR: S28617; S28617.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >234 OPACITY PROTEIN OPA65.
 FT NON_TER 234
 SQ SEQUENCE 234 AA; 26242 MW; D66A0BA6424C2F1 CRC64;
 Query Match 25.4%; Score 221; DB 1; Length 234;
 Best Local Similarity 28.1%; Pred. No. 4e-13;
 Matches 64; Conservative 21; Mismatches 65; Indels 78; Gaps 7;
 QY 24 GFYVQADAAHA-----KASSSLGS-----AKGSPRISAGYRINDLR 61
 DB 8 GFYVQADLAAYAEIRITHDYPEPTGAKKQLSTVSDYFRNIRTRSHPRVSGYDFGGRIR 67
 QY 62 AVDYTRYK-----NKAPSTDK-----LYSTASVIYDFDTQSP 96
 DB 68 AADYARFRKWKESNSSIKKVTEDIKDNYKETKEHQENGTFRHVASLSLSTIYDFQISDK 127
 QY 97 VKPYFGARLSLRASAH-----CG-----SDSFSKTSAG 126
 DB 128 IKFYIGVRVGYGHVHQVNSVGOEITVTPKPKNGTGGSPVASTPIRAYHNRSSRLG 187
 QY 127 LGVLGVSAYVTPNVDLAGYRNYGVKNTYKNNVSGELSGAVRYKF 174
 DB 188 FGAMAGVGLDVAAPGLTLDAGYRHYHNGRLENTR-FKTHASISGLVYRF 234
 RESULT 12
 ID OPAD_NEIGO STANDARD; PRT; 243 AA.
 AC 004883;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA59 precursor (Fragment).
 GN OPAD.
 OS *Neisseria gonorrhoeae*.
 CC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 CC NCBL_TaxID=485;
 RX SEQUENCE FROM N.A.
 RP STRAIN-MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;

RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 CC "Variable opacity (Opa) outer membrane proteins account for the cell
 RT tropisms displayed by *Neisseria gonorrhoeae* for human leukocytes and
 CC epithelial cells."
 RL EMBL J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Z18938; CAA79371.1; -
 DR PIR: S28629; S28629.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 DR Outer membrane; Multigene family; Signal.
 KW NON_TER 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >243 OPACITY PROTEIN OPA59.
 FT NON_TER 243 243
 SQ SEQUENCE 243 AA; 27414 MW; 5930C73917436041 CRC64;
 Query Match 25.3%; Score 220.5; DB 1; Length 243;
 Best Local Similarity 28.3%; Pred. No. 4,6e-13;
 Matches 67; Conservative 23; Mismatches 60; Indels 87; Gaps 7;
 QY 24 GGYVQADLAHNA-----KASSLSGSAK-----GSPRISAGYRINDLR 61
 DB 8 GGYVQADLAHNAVEHITHDYPEPTGKKDKISTVSDYRNIRTHSHPRVSGYDFGWMRI 67
 QY 62 AVDYTRYK-----NYKAPSTDFK-----LYSIGASV 87
 DB 68 AADYARIRKNNKNNKYSVNIKELRLNDNANGSGSHNITKRTKEHRENGTFHAASLGLS 127
 QY 88 YVDFTQSPVKPYFGARLSL-----NRASA-----HLGGS 117
 DB 128 YVDFTQSPVKPYFGARLSL-----NRASA-----HLGGS 117
 QY 118 DSFSKTSAGLGVLAGSYAVTPNDLDAGRYNYGKNTYKNNVNSGELSGAVRYKF 174
 DB 188 HESRSISLGGFAGVAGVGDITPNTLDAGRYHNMGRLENTFRTHEASLGVRVRF 243
 RESULT 13
 OPA1_NEIGO
 ID OPA1_NEIGO STANDARD: PRT; 244 AA.
 AC 004877;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA54 precursor (Fragment).
 GN OPA1.
 OS *Neisseria gonorrhoeae*.
 CC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.
 CC NCBL_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254.
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 RT tropisms displayed by *Neisseria gonorrhoeae* for human leukocytes and
 RT epithelial cells."
 RL EMBL J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE

CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
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 CC -----
 CC EMBL: Z18931; CAA79364.1; -
 DR PIR: S28622; S28622.
 DR PIR: S28618; S28618.
 DR PIR: S36332; S36332.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 DR Outer membrane; Multigene family; Signal.
 KW NON_TER 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >244 OPACITY PROTEIN OPA54.
 FT NON_TER 244 244
 SQ SEQUENCE 244 AA; 27488 MW; 968AB8603D961DD8 CRC64;
 Query Match 25.3%; Score 220; DB 1; Length 244;
 Best Local Similarity 28.2%; Pred. No. 5,2e-13;
 Matches 67; Conservative 23; Mismatches 60; Indels 88; Gaps 7;
 QY 24 GGYVQADLAHNA-----KASSLSGSAK-----GSPRISAGYRINDLR 61
 DB 8 GGYVQADLAHNAVEHITHDYPEPTGKKDKISTVSDYRNIRTHSHPRVSGYDFGWMRI 67
 QY 62 AVDYTRYK-----NYKAPSTDFK-----LYSIGASV 86
 DB 68 AADYARIRKNNKNNKYSVNIKELRLNDNANGSGSHNITKRTKEHRENGTFHAASLGLS 127
 QY 87 YVDFTQSPVKPYFGARLSL-----NRASA-----HLGGS 116
 DB 128 YVDFTQSPVKPYFGARLSL-----NRASA-----HLGGS 116
 QY 117 DSFSKTSAGLGVLAGSYAVTPNDLDAGRYNYGKNTYKNNVNSGELSGAVRYKF 174
 DB 188 HESRSISLGGFAGVAGVGDITPNTLDAGRYHNMGRLENTFRTHEASLGVRVRF 244
 RESULT 14
 OPA2_NEIGO
 ID OPA2_NEIGO STANDARD: PRT; 234 AA.
 AC P11297;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Opacity protein OPA2 precursor (Fragment).
 GN OPA2.
 OS *Neisseria gonorrhoeae*.
 CC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.
 CC NCBL_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87002493; PubMed=3093085;
 RA Stern A., Brown M., Nickel P., Meyer T.F.;
 RT "Opacity genes in *Neisseria gonorrhoeae*: control of phase and
 RT antigenic variation."
 RL Cell 47:61-71(1986).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
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 CC -----
 DR EMBL; M14747; -; NOT_ANNOTATED_CDS.
 DR PIR; B24429; K0NH8.
 DR InterPro: IPR003394; Opacity: 1.
 DR Pfam: PF02462; Opacity: 1.
 KW Outer membrane; Multigene family; Signal.
 FT SIGNAL 1 1
 FT NON_TER <1 1 POTENTIAL.
 FT CHAIN 2 >234 OPACITY PROTEIN V28.
 FT NON_TER 234 234
 SQ SEQUENCE 234 AA; 26770 MW; 339AEB09C2FE75E4 CRC64;
 Query Match 25.2%; Score 219; DB 1; Length 234;
 Best local Similarity 28.9%; Pred. No. 6, 1e-13;
 Matches 67; Conservative 21; Mismatches 38; Indels 86; Gaps 8;
 QY 24 GFVYQADAAHA-----KASSISGSAAK-----GFSRISAGYRINDLRF 61
 DB 8 GPVQADLAAYAEHTHDYPRPTDPSKGLSTVSDYFRNIRTHSIHPRVSGYDFGGMRI 67
 QY 62 AVDYTRYK--NYKAPSTDFK-----LYSIGAVIYDFPTQS 95
 DB 68 AADYARIRKNDKSYSDIKELNKNQNRDLKTENQENGTFHVVSLGLSAVYDFKLD 127
 QY 96 PVPKPYFGARLSLRASAHLGGS--DSFSKTS----- 124
 DB 128 KFKPYIGARV---AYGHVRSIDSTKKTTEFLTAGARGTDPVSSPKNTODAHQE 183
 QY 125 --AGLGLAGVSYAVTPNVDLDAGYRNYGVKNVRSGLSAGVYK 174
 DB 184 RRVGLGVIAGVGDITPNTLDAGYRHYHMGRLNTR-FKTHASLGVRIRF 234
 RESULT 15
 OP66_NEIGO STANDARD; PRT; 238 AA.
 ID 005033;
 AC 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA66 precursor (Fragment).
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID:485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VPI;
 RC MEDLINE=93178439; PubMed=8440254;
 RA Kuhsch E.-M., Knepper B., Kuroki T., Heuer J., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 RT epithelial cells."
 RL EMBL J. 12:641-650(1993).
 CC -!- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -!- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
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 CC -----
 DR EMBL; Z18941; CAA79374.1; -.
 DR PIR; S28619; S28619.
 DR InterPro: IPR003394; Opacity:
 DR Pfam; PF02462; Opacity: 1.

KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >238 OPACITY PROTEIN OPA66.
 FT NON_TER 238 238
 SQ SEQUENCE 238 AA; 26888 MW; B6E38AF1585263AA CRC64;
 Query Match 25.2%; Score 219; DB 1; Length 238;
 Best local Similarity 28.0%; Pred. No. 6, 2e-13;
 Matches 66; Conservative 23; Mismatches 57; Indels 90; Gaps 8;
 QY 24 GFVYQADAAHA-----KASSISGSAAK-----SPRISAGYRINDLRF 61
 DB 8 GPVQADLAAYAEHTHDYPRPTDPSKGLSTVSDYFRNIRTHSIHPRVSGYDFGGMRI 67
 QY 62 AVDYTRYK--NYKAPSTDFK-----LYSIGAVIYDFPTQS 93
 DB 68 AADYARIRKNDKSYSDIKELNKNQNRDLKTENQENGTFHVVSLGLSAVYDFKLD 127
 QY 94 QSPKPYFGARLSLRASAHLGGS--DSFSKTS----- 124
 DB 128 NDKFKPYIGARV---AYGHVRSIDSTKKTTEFLTAGARGTDPVSSPKNTODAHQE 183
 QY 125 -----AGLGLAGVSYAVTPNVDLDAGYRNYGVKNVRSGLSAGVYK 174
 DB 184 SNSIRVGLGVIAGVGDITPNTLDAGYRHYHMGRLNTR-FKTHASLGVRIRF 238
 Search completed: October 28, 2002, 16:01:13
 Job time : 7.98996 secs

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OM protein - protein search, using sw model

Run on: October 28, 2002, 15:56:04 ; Search time 19.9713 Seconds
(without alignments)
1507.218 Million cell updates/sec

Title: US-09-684-883-8
Perfect score: 870
Sequence: 1 MKKALAIALALPAALAE.....VNTVKNVRSGLSAGVRVKF 174

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL.19:**
1: SP_archaea:**
2: SP_bacteria:**
3: SP_fungi:**
4: SP_human:**
5: SP_invertebrate:**
6: SP_mammal:**
7: SP_mhc:**
8: SP_organelle:**
9: SP_phage:**
10: SP_plant:**
11: SP_rodent:**
12: SP_virus:**
13: SP Vertebrate:**
14: SP_unclassified:**
15: SP_rvirus:**
16: SP_bacteriopl:**
17: SP_archaeop:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	870	100.0	174	2	P95343
2	835	96.0	174	2	Q9RP18
3	834	95.9	174	16	P95372
4	832	95.6	174	2	Q9RP16
5	829	95.3	174	16	Q9RP17
6	828	95.2	174	2	Q9R2R1
7	825	94.8	174	2	P96943
8	813.5	93.5	175	2	P95371
9	242	27.8	256	2	Q51124
10	237	27.2	234	2	Q51129
11	237	27.2	234	2	Q07280
12	236	27.1	234	2	Q0718
13	235	27.0	234	2	Q07287
14	235	27.0	230	2	Q51125
15	233.5	26.8	230	2	Q9R9AT9
16	233.5	26.8	232	2	Q9K4T9

17	233	26.8	272	2	Q51013	Q51013 neisseria g
18	232.5	26.7	232	2	Q9R3P5	Q9R3P5 neisseria m
19	231.5	26.6	241	2	Q9AE80	Q9AE80 neisseria m
20	231	26.6	283	2	Q50943	Q50943 neisseria g
21	230.5	26.5	186	16	Q9CM19	Q9CM19 pasteurella
22	230.5	26.5	253	2	Q51303	Q51303 neisseria s
23	230.5	26.5	257	2	Q50929	Q50929 neisseria f
24	230	26.4	236	2	Q51126	Q51126 neisseria m
25	228	26.2	233	2	Q9K4T5	Q9K4T5 neisseria l
26	228	26.2	237	2	Q31176	Q31176 neisseria m
27	228	26.2	241	2	Q9K4T4	Q9K4T4 neisseria l
28	227	26.1	240	2	Q07925	Q07925 neisseria m
29	227	26.1	252	2	Q33388	Q33388 neisseria m
30	226	26.0	235	2	Q30753	Q30753 neisseria m
31	226	26.0	270	2	Q9RQV4	Q9RQV4 neisseria m
32	225.5	25.9	232	2	Q9R9A9	Q9R9A9 neisseria m
33	225.5	25.9	232	2	Q9R9A8	Q9R9A8 neisseria m
34	225.5	25.9	232	2	Q9K4T3	Q9K4T3 neisseria s
35	225	25.8	235	2	Q30752	Q30752 neisseria s
36	224.5	25.8	241	2	Q07274	Q07274 neisseria m
37	223.5	25.7	241	2	Q07912	Q07912 neisseria m
38	223	25.6	237	2	Q9K4T6	Q9K4T6 neisseria l
39	222	25.5	260	2	Q33389	Q33389 neisseria m
40	221.5	25.5	234	2	Q30759	Q30759 neisseria m
41	221.5	25.5	242	2	Q07279	Q07279 neisseria m
42	220.5	25.3	243	2	Q07278	Q07278 neisseria m
43	219.5	25.2	232	2	Q9K4T7	Q9K4T7 neisseria m
44	219	25.2	242	2	Q9K4T8	Q9K4T8 neisseria l
45	218.5	25.1	238	2	Q31172	Q31172 neisseria m

ALIGNMENTS

RESULT 1

ID	P95343	PRELIMINARY;	PRT;	174 AA.
AC	P95343			
DT	01-MAY-1997 (TREMBLrel. 03, Created)			
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	OUTER MEMBRANE PROTEIN PRECURSOR.			
OS	Neisseria gonorrhoeae.			
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=485;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=B2;			
RX	MEDLINE=99270944; PubMed=10338491;			
RA	Plante M., Cadieux N., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;			
RT	"Antigenic and molecular conservation of the gonococcal NspA			
RT	protein.";			
RL	Infect. Immun. 67:2855-2861(1999).			
DR	EMBL: U52069; AAB41581.1; -;			
DR	InterPro: IPR003394; Opacity.			
DR	Pfam: PF02462; Opacity; 1.			
KW	Signal.			
FT	SIGNAL.			
SQ	SEQUENCE 174 AA; 18337 MW; 1B558EC8A040841A CRC64;			
				POTENTIAL.
Query Match	100.0%;	Score 870;	DB 2;	Length 174;
Best Local Similarity	100.0%;	Pred. NO. 9.7e-64;		
Matches 174;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MKKALAIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSRISAGYRINDLR	60	
DB	1	MKKALAIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSRISAGYRINDLR	60	
QY	61	FAYDYTRKYNKAPSTDEKLVSIGASVYDDPTQSPVPRYFGARLSLRASAHIGGSDSF	120	
DB	61	FAYDYTRKYNKAPSTDEKLVSIGASVYDDPTQSPVPRYFGARLSLRASAHIGGSDSF	120	
QY	121	SFTSAGLGLVLAQSVYAVTPNVDLAGYRNNYGVKNTVKNVRSGLSAGVRVKF	174	

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Db 121 SKTSAGLVAGVSYAVTPNVDDAGYRYNYGVKNTVKNVRSGLSAGYRVKF 174
|||||
RESULT 2
ID 09RP18 PRELIMINARY; PRT; 174 AA.
AC 09RP18;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE SURFACE PROTEIN A.
GN NSPA.
OC Neisseria meningitidis.
OS Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=8047;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
DR EMBL: AF175676; AAD53279.1;
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity.
DR SEQUENCE 174 AA; 18357 MM; 0205AALDAB17F005 CRC64;
SQ

Query Match 96.0%; Score 835; DB 2; Length 174;
Best Local Similarity 95.4%; Pred. No. 7e-61;
Matches 166; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
| | | | |
Db 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
| | | | |
QY 61 FAVDYTRYKNKAPSTDFKLYSIGASVYIDPDTQSPVKPYFGARLSLNRAASVLDGSDSF 120
| | | | |
Db 61 FAVDYTRYKNKAPSTDFKLYSIGASVYIDPDTQSPVKPYFGARLSLNRAASVLDGSDSF 120
| | | | |
QY 121 SKTSAGLVAGVSYAVTPNVDDAGYRYNYGVKNTVKNVRSGLSAGYRVKF 174
| | | | |
Db 121 SKTSAGLVAGVSYAVTPNVDDAGYRYNYGVKNTVKNVRSGLSAGYRVKF 174
| | | | |

RESULT 3
ID 09P372 PRELIMINARY; PRT; 174 AA.
AC 09P372;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN PRECURSOR.
GN NSPA OR NMA0862.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487; 65699;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=24063;
RA Martin D., Cadieux N., Hamel J., Rioux C., Brodeur B.R.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN 121
DE SEQUENCE FROM N.A.
RC STRAIN=24491 / SEROGROUP A / SEROTYPE 4A;
RC MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies K.M., Davis P., Devlin K., Felwell T., Hamlin N., Holroyd S.,
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;

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RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis 22491."
RL Nature 404:502-506(2000).
DR EMBL: U52068; AAB41580.1;
DR EMBL: AL162754; CAB4143.1;
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity.
DR Signal: Complete proteome.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 174 AA; 18355 MM; EBA4A1ADA4F6F009 CRC64;

Query Match 95.9%; Score 834; DB 16; Length 174;
Best Local Similarity 95.4%; Pred. No. 8.5e-61;
Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
| | | | |
Db 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
| | | | |
QY 61 FAVDYTRYKNKAPSTDFKLYSIGASVYIDPDTQSPVKPYFGARLSLNRAASVLDGSDSF 120
| | | | |
Db 61 FAVDYTRYKNKAPSTDFKLYSIGASVYIDPDTQSPVKPYFGARLSLNRAASVLDGSDSF 120
| | | | |
QY 121 SKTSAGLVAGVSYAVTPNVDDAGYRYNYGVKNTVKNVRSGLSAGYRVKF 174
| | | | |
Db 121 SKTSAGLVAGVSYAVTPNVDDAGYRYNYGVKNTVKNVRSGLSAGYRVKF 174
| | | | |

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RESULT 4
ID 09RP16 PRELIMINARY; PRT; 174 AA.
AC 09RP16;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE SURFACE PROTEIN A.
GN NSPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
DR EMBL: AF175681; AAD53284.1;
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity.
DR SEQUENCE 174 AA; 18355 MM; ECF6F38B9286800E CRC64;
SQ

Query Match 95.6%; Score 832; DB 2; Length 174;
Best Local Similarity 94.8%; Pred. No. 1.2e-60;
Matches 165; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
| | | | |
Db 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
| | | | |
QY 61 FAVDYTRYKNKAPSTDFKLYSIGASVYIDPDTQSPVKPYFGARLSLNRAASVLDGSDSF 120
| | | | |
Db 61 FAVDYTRYKNKAPSTDFKLYSIGASVYIDPDTQSPVKPYFGARLSLNRAASVLDGSDSF 120
| | | | |
QY 121 SKTSAGLVAGVSYAVTPNVDDAGYRYNYGVKNTVKNVRSGLSAGYRVKF 174
| | | | |
Db 121 SKTSAGLVAGVSYAVTPNVDDAGYRYNYGVKNTVKNVRSGLSAGYRVKF 174
| | | | |

RESULT 5
ID 09RP17 PRELIMINARY; PRT; 174 AA.
AC 09RP17;

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DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SURFACE PROTEIN A (OUTER MEMBRANE PROTEIN NSGA).
 GN NSPA OR NMB0663.
 OS Neisseria meningitidis, and
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 ON NCBI_TaxId=487, 491;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN-CU385;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MC58 / SEROGROUP B;
 RX MEDLINE=20175755; PubMed=10710307;
 RA Tettein H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gwin M.L., DeBoy R., Peterson J.D., Hickey E.K.,
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
 RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Yamathavan J.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58.";
 RL Science 287:1809-1815(2000).
 DR EMBL: AF175678; AAD53281.1; -;
 DR EMBL: AE002420; AAF41081.1; -;
 DR TIGR: NMB0663; -;
 DR InterPro: IPR003394; Opacity: 1.
 DR Pfam: PF02462; Opacity: 1.
 DR Complete proteome.
 SQ SEQUENCE 174 AA; 18397 MW; EBB02767DDCE109 CRC64;

Query Match 95.3%; Score 829; DB 16; Length 174;
 Best Local Similarity 94.8%; Pred. No. 2.2e-60;
 Matches 165; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKKALALIALPAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASVYDFPTQSPVKPYFGARLSLNRAHAGGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASVYDFPTQSPVKPYFGARLSLNRAHAGGSDSF 120
 QY 121 SKTSAGLGVLGVSVAATPVNDLDAGYRNYVGKNTVKNVRSGLSAGYRKF 174
 DB 121 SKTSAGLGVLGVSVAATPVNDLDAGYRNYVGKNTVKNVRSGLSAGYRKF 174
 QY 121 SQTSTGLGVLGVSVAATPVNDLDAGYRNYVGKNTVKNVRSGLSAGYRKF 174

RESULT 6
 Q9R2R1 PRELIMINARY; PRT; 174 AA.
 AC Q9R2R1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE SURFACE PROTEIN A.
 GN NSPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 ON NCBI_TaxId=487;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN-M136, AND B2332;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A

RT among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 DR EMBL: AF175679; AAD53282.1; -;
 DR EMBL: AF175677; AAD53280.1; -;
 DR InterPro: IPR003394; Opacity: 1.
 DR Pfam: PF02462; Opacity: 1.
 SQ SEQUENCE 174 AA; 18385 MW; ECF6F3949286910E CRC64;

Query Match 95.2%; Score 828; DB 2; Length 174;
 Best Local Similarity 94.3%; Pred. No. 2.6e-60;
 Matches 164; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKKALALIALPAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASVYDFPTQSPVKPYFGARLSLNRAHAGGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASVYDFPTQSPVKPYFGARLSLNRAHAGGSDSF 120
 QY 121 SKTSAGLGVLGVSVAATPVNDLDAGYRNYVGKNTVKNVRSGLSAGYRKF 174
 DB 121 SQTSTGLGVLGVSVAATPVNDLDAGYRNYVGKNTVKNVRSGLSAGYRKF 174

RESULT 7
 P96943 PRELIMINARY; PRT; 174 AA.
 AC P96943;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE OUTER MEMBRANE PROTEIN PRECURSOR.
 GN NSPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 ON NCBI_TaxId=487;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN-608B;
 RX MEDLINE=97149429; PubMed=8996237;
 RA Martin D., Cadieux N., Hamel J., Brodeur B.R.;
 RT "Costimulation of T cell activation by integrin-associated protein
 (CD47) is an adhesion-dependent, CD28-independent signaling pathway";
 RL J. Exp. Med. 185:1-11(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NGP165, M986, AND NG6/88;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 DR EMBL: U52066; AAC36000.1; -;
 DR EMBL: AF175683; AAD53286.1; -;
 DR EMBL: AF175680; AAD53283.1; -;
 DR EMBL: AF175682; AAD53285.1; -;
 DR InterPro: IPR003394; Opacity: 1.
 DR Pfam: PF02462; Opacity: 1.
 DR Signal.
 FT SIGNAL.
 SQ SEQUENCE 174 AA; 18425 MW; EBB02767DDCE109 CRC64;

Query Match 94.8%; Score 825; DB 2; Length 174;
 Best Local Similarity 94.3%; Pred. No. 4.6e-60;
 Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKKALALIALPAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASVYDFPTQSPVKPYFGARLSLNRAHAGGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASVYDFPTQSPVKPYFGARLSLNRAHAGGSDSF 120

QY 121 SKTSAGLGLAGVSYAVTPNVLDAGYRKNYGVKNTVKNVSGELSGAGYRVKF 174
 Db 121 SQTSGGLAGVLAGVSYAVTPNVLDAGYRKNYGVKNTVKNVSGELSGAGYRVKF 174

RESULT 8

P95371 PRELIMINARY; PRT; 175 AA.
 ID P95371; AC P95371;
 DT 01-MAY-1997 (TREMblrel. 03, Created)
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE OUTER MEMBRANE PROTEIN PRECURSOR.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MCH 88;
 RA MEDLINE=9386904; PubMed=10456958;
 RA Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
 RT "Bactericidal and cross-protective activities of a monoclonal antibody
 directed against Neisseria meningitidis NSP4 outer membrane protein.";
 RL Infect. Immun. 67:4955-4959(1999).
 DR EMBL; U52067; AAB41579.1; -;
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity; 1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 175 AA; 18572 MW; DIEAF2FF5CC2FEA CRC64;

Query Match 93.5%; Score 813.5; DB 2; Length 175;
 Best Local Similarity 93.7%; Pred. No. 4e-59;
 Matches 164; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKKASSISGASGESPRIISAGYRINDLR 60
 Db 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKKASSISGASGESPRIISAGYRINDLR 60
 QY 61 FAVDYTRKKNYK-APSTDFKLSIGASYIDFDQSPVKPFPGARLSLNRSASHLGSSDS 119
 Db 61 FAVDYTRKKNYKQVPSDFKLSIGASAIYDFDQSPVKPFLGKRLSLNRSASVDFNDS 120
 QY 120 FSKTSAGLGLAGVSYAVTPNVLDAGYRKNYGVKNTVKNVSGELSGAGYRVKF 174
 Db 121 FSKTSAGLGLAGVSYAVTPNVLDAGYRKNYGVKNTVKNVSGELSGAGYRVKF 175

RESULT 9

Q51124 PRELIMINARY; PRT; 256 AA.
 ID Q51124; AC Q51124;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE OPACITY OUTERMEMBRANE PROTEIN (FRAGMENT).
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=24197;
 RA MEDLINE=98129089; PubMed=9467908;
 RA Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecek B.,
 RA Heckels J.E., Cannon J.G., Achtman M.;
 RT "Recombinational reassortment among opa genes from ET-37 complex
 Neisseria meningitidis isolates of diverse geographical origins.";
 RL Microbiology 144:157-166(1998).
 DR EMBL; U77255; AAC46101.1; -;
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity; 1.

FT NON_TER 1
 SQ SEQUENCE 256 AA; 28335 MW; 9D41C6079C6DD13F CRC64;

Query Match 27.8%; Score 242; DB 2; Length 256;
 Best Local Similarity 28.3%; Pred. No. 3.2e-12;
 Matches 69; Conservative 31; Mismatches 66; Indels 78; Gaps 7;

QY 8 LIALPALPAALAEAGSGFYVQADAAHAKKASSISGASGESPRIISAGYRINDLR 47
 Db 14 LPSAQAQASSESGHGPYVQADLAVALMERITHDPKATGANTTSVDYFNTIAHSIH 73
 QY 48 PRISAGYRINDLRFAVDYTRK-----NYKADSTPK-----LYS 82
 Db 74 PRVSVGYDFGGRKADYASRYKWKESNSTKKYTEDIANRYKETEKGNGSFFHAAS 133
 QY 83 IGASVYDFDQSPVKPFPGARLSLNR-----ASAHIG----- 116
 Db 134 LGLSALYDFKLDKREKPYIGARVAIGHVKHGVSEFTKTTVTSKPTATSPGGPIQTD 193
 QY 117 -----SDSFKTSAGLGLAGVSYAVTPNVLDAGYRKNYGVKNTVKNVSGELSGAGY 170
 Db 194 PSKPPYHESHSSISGLGIAGVGFDPKLLDGYRHHMGRLENR-FKTHEVSLGM 252
 QY 171 RYKF 174
 Db 253 RYKF 256

RESULT 10

O9R719 PRELIMINARY; PRT; 234 AA.
 ID O9R719; AC O9R719;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE OPACITY PROTEIN (FRAGMENT).
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=23906;
 RA MEDLINE=98010345; PubMed=9350862;
 RA Morelli G., Malorny B., Mueller K., Sellar A., Wang J., del Valle J.,
 RA Achtman M.;
 RT "Clonal descent and microevolution of Neisseria meningitidis during 30
 years of epidemic spread.";
 RL Mol. Microbiol. 25:1047-1064(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3926;
 RA Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Linn B.,
 RA Popovic T., Schuurman I.G.A., Adegbola R.A., Zurch K., Gagneux S.,
 RA Platonov A.E., Riou J.Y., Caugant D.A., Nicolas P., Achtman M.;
 RT "Fit genotypes and escape variants of subgroup III Neisseria
 meningitidis during the pandemics of epidemic meningitis.";
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF001194; AAC32715.1; -;
 DR EMBL; AJ292235; CAC36358.1; -;
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity; 1.
 FT NON_TER 1
 SQ SEQUENCE 234 AA; 26161 MW; F97142F463136EC1 CRC64;

Query Match 27.2%; Score 237; DB 2; Length 234;
 Best Local Similarity 28.9%; Pred. No. 7.3e-12;
 Matches 67; Conservative 29; Mismatches 62; Indels 74; Gaps 8;

QY 16 AALAEAG-SGFYVQADAAH-----AKASSISGASGESPRIISAGY 54
 Db 4 AASEGSRSPYVQADLAVALMERITHDPKATGANTTSVDYFNTIAHSIHPRVSVGY 63

OY 55 RINDRFAVDYTRK-----NYKAPSTDFK-----LYSIGASVI 88
 DB 64 DFGDWRIADYASYRKWKESNYSKVTEFKHONGNKQEDKTEHOGNGSFHATSSLGSAI 123
 OY 89 YDFDQSPVKPYFGARLSLNR-----ASHLGG-----SDSFSK 122
 DB 124 YDFKLNKDFKPYIGVRAVGHVAKHGVHSVESKTTVTNNNGGVPPOGPTPKPAYHSHSI 183
 OY 123 TSAGLGVLGVSAYATVPNDLDAGRYNNYGVKNTVKNVSGELSGAGVRYKF 174
 DB 184 SSVGLGVLAGVGFDTLPKLTLDGTGRYHNMGRLENT-R-FKTHEVSLGMRHYF 234

RESULT 11

ID 007280 PRELIMINARY: PRT: 234 AA.

AC 007280;
 DT 01-JUL-1997 (TREMblrel. 04, Created)
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE OPACITY PROTEIN (FRAGMENT).
 GN OPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NCBI_TaxId=487;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=23524;
 RX MEDLINE=98010345; PubMed=9350862;
 RA Morelli G., Malorny B., Muller K., Sella A., Wang J.F., del Valle J.,
 Achtmann M.;
 RT "Clonal descent and microevolution of Neisseria meningitidis during 30
 years of epidemic spread."
 RL Mol. Microbiol. 25:1047-1064(1997).
 DR EMBL: AF001195; AAC32716.1; -
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 FT NON_TER 1
 SQ SEQUENCE 234 AA; 26134 MW; 005AD356B93BCC50 CRC64;

Query Match 27.0%; Score 237; DB 2; Length 234;
 Best Local Similarity 28.9%; Pred. No. 7.3e-12;

Matches 67; Conservative 29; Mismatches 62; Indels 74; Gaps 8;

OY 16 AALAEAG-SGFYVQADAAH-----AKASSLSGS-----AKGSPRISAGY 54
 DB 4 AASEDSRSPTVQADLAIAERITHDYQATGANNSTVSDYFRNIRAHSHIPRVSGY 63
 OY 55 RINDRFAVDYTRK-----NYKAPSTDFK-----LYSIGASVI 88
 DB 64 DFGDWRIADYASYRKWKESNYSKVTEFKHONGNKQEDKTEHOGNGSFHATSSLGSAI 123
 OY 89 YDFDQSPVKPYFGARLSLNR-----ASHLGG-----SDSFSK 122
 DB 124 YDFKLNKDFKPYIGVRAVGHVAKHGVHSVESKTTVTNNNGGVPPOGPTPKPAYHSHSI 183
 OY 123 TSAGLGVLGVSAYATVPNDLDAGRYNNYGVKNTVKNVSGELSGAGVRYKF 174
 DB 184 SSVGLGVLAGVGFDTLPKLTLDGTGRYHNMGRLENT-R-FKTHEVSLGMRHYF 234

RESULT 12

ID 09R718 PRELIMINARY: PRT: 234 AA.

AC 09R718;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE OPACITY PROTEIN (FRAGMENT).
 GN OPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NCBI_TaxId=487;

RM 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-B1;
 RX MEDLINE=98010345; PubMed=9350862;
 RA Morelli G., Malorny B., Muller K., Sella A., Wang J.F., del Valle J.,
 Achtmann M.;
 RT "Clonal descent and microevolution of Neisseria meningitidis during 30
 years of epidemic spread."
 RL Mol. Microbiol. 25:1047-1064(1997).
 DR EMBL: AF001195; AAC32717.1; -
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 FT NON_TER 1
 SQ SEQUENCE 234 AA; 26191 MW; F01D3B9163066171 CRC64;

Query Match 27.1%; Score 236; DB 2; Length 234;
 Best Local Similarity 28.9%; Pred. No. 8.8e-12;

Matches 67; Conservative 28; Mismatches 63; Indels 74; Gaps 8;

OY 16 AALAEAG-SGFYVQADAAH-----AKASSLSGSAGK-----FSPRISAGY 54
 DB 4 AASEDSRSPTVQADLAIAERITHDYQATGANNSTVSDYFRNIRAHSHIPRVSGY 63
 OY 55 RINDRFAVDYTRK-----NYKAPSTDFK-----LYSIGASVI 88
 DB 64 DFGDWRIADYASYRKWKESNYSKVTEFKHONGNKQEDKTEHOGNGSFHATSSLGSAI 123
 OY 89 YDFDQSPVKPYFGARLSLNR-----ASHLGG-----SDSFSK 122
 DB 124 YDFKLNKDFKPYIGVRAVGHVAKHGVHSVESKTTVTNNNGGVPPOGPTPKPAYHSHSI 183
 OY 123 TSAGLGVLGVSAYATVPNDLDAGRYNNYGVKNTVKNVSGELSGAGVRYKF 174
 DB 184 SSVGLGVLAGVGFDTLPKLTLDGTGRYHNMGRLENT-R-FKTHEVSLGMRHYF 234

RESULT 13

ID 007287 PRELIMINARY: PRT: 234 AA.

AC 007287;
 DT 01-JUL-1997 (TREMblrel. 04, Created)
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE OPACITY PROTEIN (FRAGMENT).
 GN OPA OR OPAB.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NCBI_TaxId=487;

OY 11
 DB 124 YDFKLNKDFKPYIGVRAVGHVAKHGVHSVESKTTVTNNNGGVPPOGPTPKPAYHSHSI 183
 OY 123 TSAGLGVLGVSAYATVPNDLDAGRYNNYGVKNTVKNVSGELSGAGVRYKF 174
 DB 184 SSVGLGVLAGVGFDTLPKLTLDGTGRYHNMGRLENT-R-FKTHEVSLGMRHYF 234

RA Achtmann M., Malorny B., Muller K., Sella A., Wang J.F.,
 RT "Clonal descent and microevolution of Neisseria meningitidis during 30
 years of epidemic spread."
 RL Mol. Microbiol. 25:1047-1064(1997).
 DR EMBL: AF001204; AAC32725.1; -
 DR EMBL: AF004823; AAC32684.1; -
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 FT NON_TER 1
 SQ SEQUENCE 234 AA; 25933 MW; 61E375DD82AEE2 CRC64;

Query Match 27.0%; Score 235; DB 2; Length 234;
 Best Local Similarity 28.0%; Pred. No. 1.1e-11;
 Matches 65; Conservative 29; Mismatches 64; Indels 74; Gaps 6;

OY 16 AALAEAG-SGFYVQADAAH-----KASSLSGS-----AKGSPRISAGY 54

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DB 4 AASEDGRSPYVOADLAIAERITHDYPRKATGANNSTVSDYFRNIRAHSHIPRVSVGY 63
QY 55 RINDLRADVYTRYKKNKAPSTD-----FKLSIGASVLY 89
DB 64 DFDWMRIADYASYIRKMKESNSTNTENSETOONRIKIETGHOGNSFLNASSLSGLSALT 123
QY 90 DFDTPSPFKPEYFGARLSLNRSASHLGSDSFSKST----- 123
DB 124 DFLNKDFKRYIGARVAVGVVKKHQVSSEKTKVTSKPNCGPVKGGPTPKPAYHESNSI 183
QY 124 -SAGLGVLAVSYAVTPNVDDLADGIRYNYGKYNVKNRSGLSGVRKVF 174
DB 184 SSIIGLVIAVGVDITPKLTLDGTYRHHMGRLENTR-FKTHEVSLGVRKHF 234

RESULT 14
ID 051125 PRELIMINARY; PRT; 259 AA.
AC 051125;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DE 01-MAY-1997 (T-EMBLrel. 03, last sequence update)
DE 01-JUN-2001 (T-EMBLrel. 17, last annotation update)
DE OPACITY OUTERMEMBRANE PROTEIN (FRAGMENT).
GN OPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=24197;
RX MEDLINE=98129089; PubMed=9467908;
RA Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecek B.,
  Hecksels J.E., Cannon J.G., Achtman M.;
RT "Recombinational reassortment among opa genes from ET-37 complex
  Neisseria meningitidis isolates of diverse geographical origins.";
RL Microbiol. 144:157-166(1998).
DR EMBL; U37256; AAC46102.1; -.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
FT NON_TER 1
SQ SEQUENCE 259 AA; 28856 MW; 8E19050D51157DE3 CRC64;

Query Match 27.0%; Score 235; DB 2; Length 259;
Best Local Similarity 28.5%; Pred. No. 1.2e-11;
Matches 70; Conservative 29; Mismatches 67; Indels 80; Gaps 7;

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DT 01-MAY-2000 (T-EMBLrel. 13, last sequence update)
DE 01-DEC-2001 (T-EMBLrel. 19, last annotation update)
DE OPACITY PROTEIN (FRAGMENT).
GN OPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98010345; PubMed=9350862;
RA Morelli G., Malorny B., Muller K., Sella A., Wang J.F., del Valle J.,
  Achtman M.;
RT "Clonal descent and microevolution of Neisseria meningitidis during 30
  years of epidemic spread.";
RL Mol. Microbiol. 25:1047-1064(1997).
DR EMBL; AF031337; AAC45980.1; -.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
FT NON_TER 1
SQ SEQUENCE 230 AA; 23819 MW; 970DC4570B57A697 CRC64;

Query Match 26.8%; Score 233.5; DB 2; Length 230;
Best Local Similarity 28.6%; Pred. No. 1.4e-11;
Matches 64; Conservative 27; Mismatches 60; Indels 73; Gaps 7;

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DB 8 SPYVQADLAIAERITHDYPRKATGANNSTVSDYFRNIRAHSHIPRVSVGYDGDWRIA 67
QY 63 VDYTRYK-----NYKAPSTDCK-----LYSIGASYIDPDQSP 96
DB 68 ADYASYIRKMKESNSKKTTERKHQNGKQEDKTEHQNGSFHATSSLSGLSALTDFKLDK 127
QY 97 VKPYFGARLSLNR-----ASHLG-----SDSFKTSAGLGLV 130
DB 128 FKPYGVAVAGVKKHQVHSVESKTTVTNNGGPVPGPTPKPAYHESHSISSVGLGI 187
QY 131 AGVSYAVTPNVDDLADGIRYNYGKYNVKNRSGLSGVRKVF 174
DB 188 AGVGFDPITPKLTLDGTYRHHMGRLENTR-FKTHEVSLGVRKHF 230

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Search completed: October 28, 2002, 16:02:40
Job time : 20.9713 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 28, 2002, 16:00:44 ; Search time 103.601 Seconds

(without alignments)
591.158 Million cell updates/sec

Title: US-09-684-883-2

Perfect score: 868
Sequence: 1 MKKALVTLLALPAAALAE.....VNTKNSGELSGVRYKF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	868	100.0	174	8	US-08-406-362-2
2	868	100.0	174	22	US-09-870-759-36
3	135	15.6	170	8	US-08-479-520-20
4	135	15.6	170	8	US-08-486-050-20
5	135	15.6	170	8	US-08-486-050A-20
6	135	15.6	170	13	US-08-988-444-20
7	135	15.6	170	16	US-09-217-849-20

8	135	15.6	170	18	US-09-489-850-20	Sequence 20, Appl
9	129.5	14.9	281	21	US-09-739-449-11638	Sequence 11638, A
10	129.5	14.9	281	22	US-09-803-110-11638	Sequence 11638, A
11	113.5	13.1	98	19	US-09-540-236-2245	Sequence 2245, Ap
12	109.5	12.6	187	18	US-09-489-039A-13699	Sequence 13699, Ap
13	104.5	12.0	384	19	US-09-543-681A-79922	Sequence 79922, Ap
14	101	11.6	21	24	US-10-082-014-124	Sequence 124, Ap
15	101	11.6	21	26	US-60-358-618-48	Sequence 48, Appl
16	99	11.4	217	16	US-09-252-691-9162	Sequence 9162, Ap
17	99	11.4	217	16	US-09-252-691C-9162	Sequence 9162, Ap
18	97	11.2	21	24	US-10-082-014-123	Sequence 123, Ap
19	97	11.2	21	26	US-60-358-618-47	Sequence 47, Appl
20	94.5	10.9	212	22	PCT-US02-03987-10149	Sequence 10149, A
21	94.5	10.9	212	22	US-09-815-242-10149	Sequence 10149, A
22	94.5	10.9	212	22	US-10-072-851-10149	Sequence 10149, A
23	93	10.7	190	19	US-09-543-681A-7684	Sequence 7684, Ap
24	92.5	10.7	261	16	US-09-252-991A-19759	Sequence 19759, A
25	92	10.6	225	24	US-10-015-127-13821	Sequence 2792, Ap
26	89.5	10.3	186	19	US-09-540-236-2792	Sequence 4082, Ap
27	89.5	10.3	186	26	US-60-128-476-4082	Sequence 13845, A
28	89.5	10.3	257	1	PCT-US02-03987-13845	Sequence 13845, A
29	89.5	10.3	257	22	US-09-815-242-13845	Sequence 13845, A
30	89.5	10.3	257	24	US-10-072-851-13845	Sequence 7451, Ap
31	88.5	10.2	385	18	US-09-489-039A-7451	Sequence 7451, Ap
32	88.5	10.2	180	1	PCT-US99-22918-7	Sequence 7, Appl
33	88.5	10.2	180	15	US-09-164-714-7	Sequence 7, Appl
34	88.5	10.2	573	23	US-09-952-267-3	Sequence 3, Appl
35	88.5	10.2	573	23	US-09-952-267A-3	Sequence 3, Appl
36	88	10.1	359	4	US-08-065-442-2	Sequence 2, Appl
37	88	10.1	359	8	US-08-457-997-2	Sequence 2, Appl
38	88	10.1	359	8	US-08-457-997A-2	Sequence 2, Appl
39	88	10.1	359	18	US-08-467-722-2	Sequence 2, Appl
40	88	10.1	359	18	US-09-451-184-2	Sequence 2, Appl
41	88	10.1	397	23	US-09-902-540-16267	Sequence 16267, A
42	88	10.1	610	23	US-09-952-267-11	Sequence 11, Appl
43	88	10.1	610	23	US-09-952-267A-11	Sequence 11, Appl
44	88	10.1	624	23	US-09-952-267-7	Sequence 7, Appl
45	88	10.1	624	23	US-09-952-267A-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-406-362-2
; Sequence 2, Application US/08406362
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,362
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Pharma-43

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-406-362-2

Query Match          100.0%; Score 868; DB 8; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.9e-91;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGAGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGAGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDEKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDEKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGSDSF 120
QY 121 SQTSGIGLVTCGYSAVPPNVDLDAGYRNYGKYNVKNVBSGELSVGRVKE 174
DB 121 SQTSGIGLVTCGYSAVPPNVDLDAGYRNYGKYNVKNVBSGELSVGRVKE 174

RESULT 2
US-09-870-759-36
; Sequence 36, Application US/09870759
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-09-870-759-36

Query Match          100.0%; Score 868; DB 22; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.9e-91;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 FAVDYTRYKNYKAPSTDEKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDEKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGSDSF 120
QY 121 SQTSGIGLVTCGYSAVPPNVDLDAGYRNYGKYNVKNVBSGELSVGRVKE 174
DB 121 SQTSGIGLVTCGYSAVPPNVDLDAGYRNYGKYNVKNVBSGELSVGRVKE 174

RESULT 3
US-08-479-520-20
; Sequence 20, Application US/08479520
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
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; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,520
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/105/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-479-520-20

Query Match          15.6%; Score 135; DB 8; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.1e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

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QY 46 FSPRISAGYRINDLRFAVDTRYKNYKAPSTDEK 79
DB 75 IHPKVSVDYDFEGGRADYASFRKNNNNKYVNTKELEKHNKKDLKTENQENCTFHA 134
QY 80 LYSIGASAIYDPTQSPVKPYLGARLSLNRAVD 113
DB 135 ASSIGLSAIYDFKLGKFKPYIGARAVYGHVRSID 170

RESULT 4
US-08-486-050-20
; Sequence 20, Application US/08486050
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,050
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/103/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-486-050-20

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Best Local Similarity 26.3%; Pred. No. 1,1e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

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; Sequence 20, Application US/08486050A
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/486,050A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.

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; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/103/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-486-050A-20

Query Match      15.6%; Score 135; DB 8; Length 170;
Best Local Similarity 26.3%; Pred. No. 1,1e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATTLALPAALAEAGSGFYVOADAH-----AKASSLSG-----AKG 45
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 15 SSLFSSAAQAASDRSRSPYVOADLAYAERITHDYPQATGANNTSTVSDYFRNIRAH 74
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 46 FSPRISAGYRINDREFAVDYTRYKNY-----KAPSTDCK 79
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 75 IHPRVSVGYDPGWRRIADYASRYKMNKNKYSVNTRKLENNKKNKDKLTENGCTFHA 134
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 80 LYSIGASAIYDPTQSPVKPYLGRLSLN--RASVD 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 135 ASLSGLSAIYDFKLGKFKRPYIGARVAAGVHRHSID 170
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
US-08-988-444-20
; Sequence 20, Application US/08988444
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,444
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,050
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/103/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids

```

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-988-444-20

Query Match 15.6%; Score 135; DB 13; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.1e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLIALPAALAEAGSGFYVQADAAH-----AKASSLSG-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYVQADLAAERITHDYPOATGANNSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFVAVYTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDFGGMRIADYASYRKNNKYSVNTKELENKHNKKDKLTENQNGTFFHA 134
QY 80 LYSIGASATYDDTQSPVRYGARLSLN--RASVD 113
DB 135 ASSLSGSAIYDFKLGKFKRPYIGARVAGVHRHSID 170

RESULT 7
US-09-217-849-20
Sequence 20, Application US/09217849

GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,849
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-09-217-849-20

Query Match 15.6%; Score 135; DB 16; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.1e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLIALPAALAEAGSGFYVQADAAH-----AKASSLSG-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYVQADLAAERITHDYPOATGANNSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFVAVYTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDFGGMRIADYASYRKNNKYSVNTKELENKHNKKDKLTENQNGTFFHA 134
QY 80 LYSIGASATYDDTQSPVRYGARLSLN--RASVD 113
DB 135 ASSLSGSAIYDFKLGKFKRPYIGARVAGVHRHSID 170

RESULT 8
US-09-489-850-20
Sequence 20, Application US/09489850

GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/489,850
FILING DATE: 24-Jan-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/988,444
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-489-850-20

Query Match 15.6%; Score 135; DB 18; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.1e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLIALPAALAEAGSGFYVQADAAH-----AKASSLSG-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYVQADLAAERITHDYPOATGANNSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFVAVYTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDFGGMRIADYASYRKNNKYSVNTKELENKHNKKDKLTENQNGTFFHA 134

Query Match 14.9%; Score 129.5; DB 22; Length 281;

Matches 51; Conservative 26; Mismatches 78; Indels 47; Gaps

Matches 51; Conservative 26; Mismatches 78; Indels 47; Gaps

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OM protein - protein search, using sw model

Run on: October 28, 2002, 16:01:19 ; Search time 35.6987 Seconds

(without alignments)
1465.185 Million cell updates/sec

Title: US-09-684-883-2

Perfect score: 868
Sequence: 1 MKKALATIALALPAALAE.....VNTYKNVRSGLSVGRVKE 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1112697 seqs, 300604653 residues

Total number of hits satisfying chosen parameters: 1112697

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/paa/PCF_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/PCF_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
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6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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8: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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10: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
12: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	174	9	US-09-684-883-2
2	854	98.4	174	9	US-09-684-883-6
3	838.5	96.6	175	9	US-09-684-883-30
4	825	95.0	174	9	US-09-684-883-8
5	824.5	95.0	175	9	US-09-684-883-4
6	133	15.3	25	9	US-10-203-942-9
7	94	10.8	353	11	US-10-219-999-45753
8	89	10.3	187	11	US-10-219-999-55699
9	89	10.3	229	11	US-09-791-537-117254
10	88.5	10.2	576	9	US-09-791-537-117254
11	88.5	10.2	765	9	US-09-791-537-117254
12	87	10.0	16	9	US-09-684-883-15
13	87	10.0	500	9	US-09-990-004A-149
14	87	10.0	500	11	US-10-219-220-149
15	86	9.9	213	9	US-09-791-537-112202
16	85.5	9.9	339	9	US-09-513-966A-67258
17	85.5	9.9	534	9	US-09-513-966A-7956
18	84	9.7	165	9	US-09-540-209B-7537
19	83.5	9.6	576	9	US-09-458-180-2
20	83	9.6	364	9	US-09-545-199F-151

21	82	9.4	433	9	US-09-791-537-118678	Sequence 118678,
22	81	9.3	15	9	US-09-684-883-23	Sequence 23, Appl
23	80.5	9.3	330	9	US-09-120-051C-47	Sequence 47, Appl
24	80.5	9.3	330	9	US-09-120-051D-47	Sequence 47, Appl
25	80.5	9.3	573	9	US-09-540-209B-5271	Sequence 5271, Ap
26	80.5	9.3	695	9	US-09-791-537-24508	Sequence 24508, A
27	80.5	9.3	792	11	US-10-179-131-8424	Sequence 8424, Ap
28	80	9.2	316	9	US-09-513-966A-67259	Sequence 67259, A
29	80	9.2	511	9	US-09-513-966A-7957	Sequence 7957, Ap
30	80	9.2	511	9	US-09-513-966A-39219	Sequence 39219, A
31	79.5	9.2	369	9	US-09-545-199F-153	Sequence 153, App
32	79.5	9.2	421	9	US-09-791-537-114829	Sequence 114829,
33	79.5	9.2	431	9	US-09-791-537-28171	Sequence 28171, A
34	79.5	9.2	516	9	US-09-791-537-29175	Sequence 29175, A
35	79	9.1	15	9	US-09-684-883-18	Sequence 18, Appl
36	79	9.1	264	9	US-09-956-508A-4	Sequence 4, Appl
37	79	9.1	293	11	US-10-059-964-54	Sequence 54, Appl
38	79	9.1	427	9	US-09-540-209B-6145	Sequence 6145, Ap
39	79	9.1	1114	11	US-10-069-799-1	Sequence 1, Appl
40	78.5	9.0	189	11	US-10-108-260A-3443	Sequence 3443, Ap
41	78.5	9.0	189	11	US-10-108-260A-3443	Sequence 3443, Ap
42	78.5	9.0	332	11	US-10-193-002-53	Sequence 53, Appl
43	78.5	9.0	652	11	US-10-193-002-350	Sequence 350, App
44	78.5	9.0	802	11	US-10-193-002-209	Sequence 209, App
45	78.5	9.0	802	11	US-10-193-002-346	Sequence 346, App

ALIGNMENTS

RESULT 1
US-09-684-883-2
Sequence 2, Application US/09684883
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Martin, Denis
Hamel, Josee
Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-684-883-2

Query Match 100.0%; Score 868; DB 9; Length 174;
Best Local Similarity 100.0%; Pred. No. 7.4e-83;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSISGAKGSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSISGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRKKNKAPSTDFKLSIGASAIYDFDTPQSPVKPYLGARLSINRASVDLGSDSF 120
DB 61 FAVDYTRKKNKAPSTDFKLSIGASAIYDFDTPQSPVKPYLGARLSINRASVDLGSDSF 120
QY 121 SQTSGIGLVLAGSYAVTPNVLDAGYRNYIGKVTYKKNVRSGLSVGYRVKF 174
DB 121 SQTSGIGLVLAGSYAVTPNVLDAGYRNYIGKVTYKKNVRSGLSVGYRVKF 174

RESULT 2
US-09-684-883-6
Sequence 6, Application US/09684883
GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

Hamel, Denise
Hamel, Josee
Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997

APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995

APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-684-883-6

Query Match 98.4%; Score 854; DB 9; Length 174;
Best Local Similarity 98.3%; Pred. No. 2.2e-81;
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSISGAKGSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSISGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRKKNKAPSTDFKLSIGASAIYDFDTPQSPVKPYLGARLSINRASVDLGSDSF 120
DB 61 FAVDYTRKKNKAPSTDFKLSIGASAIYDFDTPQSPVKPYLGARLSINRASVDLGSDSF 120
QY 121 SQTSGIGLVLAGSYAVTPNVLDAGYRNYIGKVTYKKNVRSGLSVGYRVKF 174
DB 121 SQTSGIGLVLAGSYAVTPNVLDAGYRNYIGKVTYKKNVRSGLSVGYRVKF 174

RESULT 3
US-09-684-883-30

Sequence 30, Application US/09684883
GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

Hamel, Denise
Hamel, Josee
Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997

APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995

APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear

STRANDEDNESS: <unknown>

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-684-883-30

Query Match 96.6%; Score 838.5; DB 9; Length 175;
Best Local Similarity 97.1%; Pred. No. 9.2e-80;
Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

[illegible]

[illegible]


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QY      19 AEGASGEYVQADA-----AHAKASSSLCS-AKGFSPRISA-GYRINDLRFAVDYTR 67
      |      : |      |||      :|| : ||:      || ||:|      :|| |

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997

APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 04/998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
STRAIN: 608B
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-684-883-15

Query Match 10.0%; Score 87; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FAVDYTRYKNYKAPST 76
DB 1 FAVDYTRYKNYKAPST 16

RESULT 13
US-09-990-004A-149
Sequence 149, Application US/09990004A
GENERAL INFORMATION:
APPLICANT: Flihm, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Methods for Modulating Cellular Development and Programmed Cell De
FILE REFERENCE: 11000.103861
CURRENT APPLICATION NUMBER: US/09/990,004A
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 09/327,373
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 149
LENGTH: 500
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-990-004A-149

Query Match 10.0%; Score 87; DB 9; Length 500;
Best Local Similarity 23.7%; Pred. No. 2.1;
Matches 41; Conservative 19; Mismatches 81; Indels 32; Gaps 4;

QY 4 ALATLIALPALAALAEASGFYQADAAHAKASSLSGSAKGFSPRISAGYRI-----56
DB 32 AAVALALALALTITIASALDMSIVSYDRAGDSSSSSSWRSDDEVMAYYESWLAKHGK 91
QY 57 -----NDLRFVAV--DYTRYKNYKAPSTDEKLYSIGASAIYEDTQSPYKPYLGARLSL 107
DB 92 AYNALGEKERKFFQYFKNLRFIDHNGGD--RYTVGLNGPADLTNEYSRSMYLGARMOR 150
QY 108 NRASVDLGSDSFSQTSIGLVLTGVSAYTPNVDLDAGYRYNYIGKYNVYKN 160
DB 151 SGRRLGARSD-----RYAVALAGELPASVDMRREGAVVDVKD 188

RESULT 14
US-10-219-220-149
Sequence 149, Application US/10219220

GENERAL INFORMATION:
APPLICANT: Flihm, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
FILE REFERENCE: 11000.102261
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. 09/325,932
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 299
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 149
LENGTH: 500
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-10-219-220-149

Query Match 10.0%; Score 87; DB 11; Length 500;
Best Local Similarity 23.7%; Pred. No. 2.1;
Matches 41; Conservative 19; Mismatches 81; Indels 32; Gaps 4;

QY 4 ALATLIALPALAALAEASGFYQADAAHAKASSLSGSAKGFSPRISAGYRI-----56
DB 32 AAVALALALALTITIASALDMSIVSYDRAGDSSSSSSWRSDDEVMAYYESWLAKHGK 91
QY 57 -----NDLRFVAV--DYTRYKNYKAPSTDEKLYSIGASAIYEDTQSPYKPYLGARLSL 107
DB 92 AYNALGEKERKFFQYFKNLRFIDHNGGD--RYTVGLNGPADLTNEYSRSMYLGARMOR 150
QY 108 NRASVDLGSDSFSQTSIGLVLTGVSAYTPNVDLDAGYRYNYIGKYNVYKN 160
DB 151 SGRRLGARSD-----RYAVALAGELPASVDMRREGAVVDVKD 188

RESULT 15
US-09-791-537-112202
Sequence 112202, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Blomomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 112202
LENGTH: 213
TYPE: PRT
ORGANISM: Brucella canis
US-09-791-537-112202

Query Match 9.9%; Score 86; DB 9; Length 213;
Best Local Similarity 25.3%; Pred. No. 0.85;
Matches 47; Conservative 32; Mismatches 71; Indels 34; Gaps 9;

QY 14 PAALAEASGFYQADAAHAKASSLSGSAKGFSPRISAGYRI-----GYRINDLRFVAVDYTRYK 69
DB 41 PYSNAGGTGTLGLYIGKNNKAK--TSTVGSINPDDMKAGAFAGWNPQKQIYVYEGDAGY 99
QY 70 NYKAPSTD-----FKLYSIGASAIYEDTQSPYKPYL-----GARLSNRASVDLGGS 117
DB 100 SWAKSKSGDLEVKQGF--GSLRARVGYDL--NPWMPYLTGAGISQIKLN-----NGL 149
QY 118 DSFSQTSIGLVLTGVSAYTPNVDLDAGYRI-----NYIGKYNVYKN--VRSGLSNGV 170
DB 150 DGSKFRVGTAGAGLEAKLDNIIIGRVEYRYTOYSNKNYDLAGTTVYNNKLDODIRVGI 209
QY 171 RYKF 174

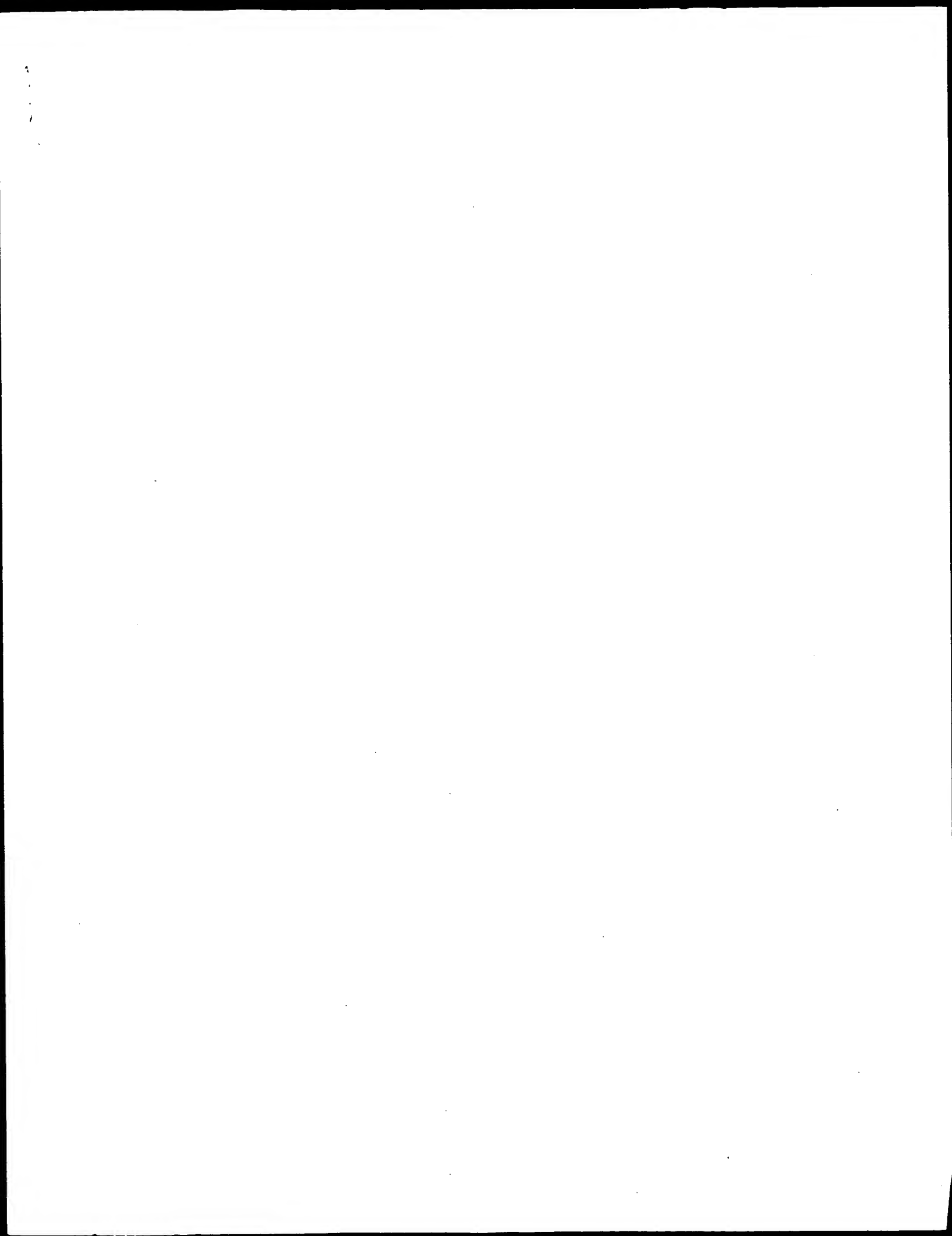
Tue Oct 29 09:23:07 2002

us-09-684-883-2.rapn

Page 7

Db 210 GYKF 213

Search completed: October 28, 2002, 16:13:49
Job time : 36.6987 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 28, 2002, 16:00:44 ; Search time 104.197 Seconds

(without alignments)
591.158 Million cell updates/sec

Title: US-09-684-883-4

Sequence: 1 MKKALALIALALPAAIAE.....VNTKYNRSGELAGVYKF 175

Scoring table:

BLOSUM62
Gapd 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/1/paa/PCMS.COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06.COMB.pep.*
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11: /cgn2_6/ptodata/1/paa/US087.COMB.pep.*
12: /cgn2_6/ptodata/1/paa/US088.COMB.pep.*
13: /cgn2_6/ptodata/1/paa/US089.COMB.pep.*
14: /cgn2_6/ptodata/1/paa/US090.COMB.pep.*
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22: /cgn2_6/ptodata/1/paa/US098.COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US099.COMB.pep.*
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26: /cgn2_6/ptodata/1/paa/US60.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	824.5	94.3	174	8	US-08-406-362-2
2	824.5	94.3	174	22	US-09-870-759-36
3	138.5	15.8	170	8	US-08-479-520-20
4	138.5	15.8	170	8	US-08-486-050-20
5	138.5	15.8	170	8	US-08-486-050A-20
6	138.5	15.8	170	13	US-08-988-444-20
7	138.5	15.8	170	16	US-09-217-849-20

8	138.5	15.8	170	18	US-09-489-850-20	Sequence 20, Appl
9	128	14.6	281	21	US-09-739-449-11638	Sequence 11638, A
10	128	14.6	281	22	US-09-803-110-11638	Sequence 11638, A
11	116	13.3	187	18	US-09-489-039A-13699	Sequence 13699, A
12	114.5	13.1	98	19	US-09-540-236-2245	Sequence 2245, Ap
13	107.5	12.3	190	19	US-09-543-681A-7684	Sequence 7684, Ap
14	104	11.9	487	17	US-09-328-352-5331	Sequence 5331, Ap
15	101.5	11.6	217	16	US-09-252-691-9162	Sequence 9162, Ap
16	101.5	11.6	217	16	US-09-252-691C-9162	Sequence 9162, Ap
17	101	11.6	21	24	US-10-082-014-123	Sequence 123, Ap
18	101	11.6	21	26	US-09-358-618-47	Sequence 47, Appl
19	99.5	11.4	257	1	PCT-US02-03987-13845	Sequence 13845, A
20	99.5	11.4	257	22	US-09-815-242-13845	Sequence 13845, A
21	99.5	11.4	257	24	US-10-072-851-13845	Sequence 13845, A
22	98.5	11.3	643	17	US-09-328-352-5146	Sequence 5146, Ap
23	97	11.1	21	24	US-10-082-014-124	Sequence 124, App
24	97	11.1	21	26	US-09-358-618-48	Sequence 48, Appl
25	97	11.1	384	19	US-09-543-681A-7922	Sequence 7922, Ap
26	95.5	10.9	212	1	PCT-US02-03987-10149	Sequence 10149, A
27	95.5	10.9	212	22	US-09-815-242-10149	Sequence 10149, A
28	95.5	10.9	212	24	US-10-072-851-10149	Sequence 10149, A
29	95.5	10.9	568	7	US-08-331-393-5	Sequence 5, Appl
30	95	10.9	955	24	US-10-015-127-11706	Sequence 11706, A
31	93.5	10.7	350	14	US-09-080-025-3	Sequence 3, Appl
32	93.5	10.7	351	16	US-09-252-991A-30094	Sequence 30094, A
33	93.5	10.7	359	4	US-08-065-442-2	Sequence 2, Appl
34	93.5	10.7	359	8	US-08-457-997A-2	Sequence 2, Appl
35	93.5	10.7	359	8	US-08-457-997A-2	Sequence 2, Appl
36	93.5	10.7	359	8	US-08-457-997A-2	Sequence 2, Appl
37	93.5	10.7	359	18	US-09-451-184-2	Sequence 2, Appl
38	93.5	10.7	359	18	US-09-418-980-10	Sequence 10, Appl
39	93.5	10.7	369	19	US-09-506-078-46	Sequence 46, Appl
40	93.5	10.7	369	19	US-09-545-159C-153	Sequence 153, App
41	93.5	10.7	369	19	US-09-545-159D-153	Sequence 153, App
42	93.5	10.7	369	22	US-09-809-665A-153	Sequence 46, Appl
43	93.5	10.7	369	26	US-09-120-454-46	Sequence 46, Appl
44	90	10.3	215	18	US-09-418-980-4	Sequence 4, Appl
45	90	10.3	215	19	US-09-506-078-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-08-406-362-2
Sequence 2, Application US/08406362
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
Zip: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,362
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Pharma-43

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-406-362-2

Query Match 94.3%; Score 824.5; DB 8; Length 174;
Best Local Similarity 95.4%; Pred. No. 2e-83;
Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 MKKALALIALPAAALAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKVPSTDFELYSIGASAIYDFDTQSPVPRYLGARLSLRASVDENGSDS 120
DB 61 FAVDYTRYKNYK-APSTDRKISIGASAIYDFDTQSPVPRYLGARLSLRASVDLGSDS 119
QY 121 FSQTSIGLVAGVSYAVTPNVDLDAGRYNYIGKYNIVKVRSGELSGAVRYKF 175
DB 120 FSQTSIGLVAGVSYAVTPNVDLDAGRYNYIGKYNIVKVRSGELSGAVRYKF 174

RESULT 2

US-09-870-759-36
Sequence 36, Application US/09870759
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
LENGTH: 174
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-870-759-36

Query Match 94.3%; Score 824.5; DB 22; Length 174;
Best Local Similarity 95.4%; Pred. No. 2e-83; Mismatches 7; Indels 1; Gaps 1;
Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 MKKALALIALPAAALAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKVPSTDFELYSIGASAIYDFDTQSPVPRYLGARLSLRASVDENGSDS 120
DB 61 FAVDYTRYKNYK-APSTDFELYSIGASAIYDFDTQSPVPRYLGARLSLRASVDLGSDS 119
QY 121 FSQTSIGLVAGVSYAVTPNVDLDAGRYNYIGKYNIVKVRSGELSGAVRYKF 175
DB 120 FSQTSIGLVAGVSYAVTPNVDLDAGRYNYIGKYNIVKVRSGELSGAVRYKF 174

RESULT 3

US-08-479-520-20
Sequence 20, Application US/08479520
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,520
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/105/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-479-520-20

Query Match 15.8%; Score 138.5; DB 8; Length 170;
Best Local Similarity 26.9%; Pred. No. 1e-06;
Matches 42; Conservative 19; Mismatches 48; Indels 47; Gaps 4;

QY 6 AALIALPAAALAGSGFYVQADAAH-----AKASSLSG-----AKG 45
DB 15 SLEFSSAAQASSEDSPRYVQADLVAERITHYDPATGANNTSTVSDYRNRRAHS 74
QY 46 FSPRISAGYRINDLRFAVDYTRYKNY-----KQVPSTDFK 80
DB 75 IHPRVSVGDFGWRIRADYASYRRKMNWNNKYSVNTKELENKHNKKDKLTENGTFHA 134
QY 81 LYSIGASAIYDFDTQSPVPRYLGARLSLN--RASVD 114
DB 135 ASSLSGSAIYDFKLGKRPYIGARVAVGVHVRHSID 170

RESULT 4

US-08-486-050-20
Sequence 20, Application US/08486050
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-486-050-20

Query Match 15.8%; Score 138.5; DB 8; Length 170;
Best Local Similarity 26.9%; Pred. No. 1e-06;
Matches 42; Conservative 19; Mismatches 48; Indels 47; Gaps 4;

QY 6 AALIALPAAALAEAGSGFYVQADAAH-----AKASSLSGS-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYVQADLAFAERITHDYPQATGANNTSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KQVSTDFK 80
DB 75 IHPRVSGYDFGCGRIADYASIRKNNKYSVNTKELENKHNKKDKLTENGCTFHA 134
QY 81 LYSIGASAIYDFDTQSPVKPYIGARLSLN--RASVD 114
DB 135 ASSLSAISYDFKLKGFKPYIGARVAAGVHRHSID 170

RESULT 5
US-08-486-050A-20
Sequence 20, Application US/08486050A
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-486-050A-20

Query Match 15.8%; Score 138.5; DB 8; Length 170;
Best Local Similarity 26.9%; Pred. No. 1e-06;
Matches 42; Conservative 19; Mismatches 48; Indels 47; Gaps 4;

QY 6 AALIALPAAALAEAGSGFYVQADAAH-----AKASSLSGS-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYVQADLAFAERITHDYPQATGANNTSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KQVSTDFK 80
DB 75 IHPRVSGYDFGCGRIADYASIRKNNKYSVNTKELENKHNKKDKLTENGCTFHA 134
QY 81 LYSIGASAIYDFDTQSPVKPYIGARLSLN--RASVD 114
DB 135 ASSLSAISYDFKLKGFKPYIGARVAAGVHRHSID 170

RESULT 6
US-08-988-444-20
Sequence 20, Application US/08988444
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,444
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,050
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids

QY 81 LYSIGASATYDDTQSPVKPYTGARLSLN--RASVD 114
 DB 135 ASSLAGFLAVLTGTSAIADLYQAEPAAYDAPETVTOASGWTLDGDIYSPNKLK 170

RESULT 9
 US-09-739-449-11638

; Sequence 11638, Application US/09739449
 ; GENERAL INFORMATION:
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15490)C
 ; CURRENT APPLICATION NUMBER: US/09/739,449
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: US 09/514,000
 ; PRIOR FILING DATE: 2000-02-23
 ; NUMBER OF SEQ ID NOS: 13351
 ; SEQ ID NO 11638
 ; LENGTH: 281
 ; TYPE: PRF
 ; ORGANISM: Agrobacterium tumefaciens
 US-09-739-449-11638

Query Match 14.6%; Score 128; DB 21; Length 281;
 Best Local Similarity 22.4%; Pred. No. 3.2e-05;
 Matches 58; Conservative 28; Mismatches 89; Indels 84; Gaps 10;

QY 1 MKKALALIALAL-----PAALAE-----ASGFVQAD----- 30
 DB 1 MKKALAGFLAVLTGTSAIADLYQAEPAAYDAPETVTOASGWTLDGDIYSPNKLK 60
 QY 31 AAHAKASSLSGSAKGFSPRI-----SAGYRINDL---REAVDYTRYKNYK----- 72
 DB 61 GAHYGCGPGGYLDPTATIKDSYVIGGVGYQFNPNFRSDVTLIDYMGKSDFRGSTSGF 120
 QY 73 --QVPS-----TDFKLYSIGASATYDDTQSPVKPYTGARL-----SLNRASVDF 115
 DB 121 CGSVPGRCVSADLSLSAYTLMANAYVDLTGYGSIPTPYVGSGIGSYKWDKLRNTSCSV 180
 QY 116 NGSDSFQSTSTG-----LGLVAGSYAVTPNVDLDAGYRYNYIGKVNTY----- 159
 DB 181 NGLCGDPPTTEHGGKGRKRAIYALMAGASIDVTCNLKADIGYFRHINKGDMFAYENGCGP 240
 QY 160 ---KNVRSGLSAGRYVKF 175
 DB 241 GRDKGLYSHEVRVGRYVF 259

RESULT 10
 US-09-803-110-11638

; Sequence 11638, Application US/09803110
 ; GENERAL INFORMATION:
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15490)D
 ; CURRENT APPLICATION NUMBER: US/09/803,110
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 09/739,449
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: US 09/514,000
 ; PRIOR FILING DATE: 2000-02-23
 ; PRIOR APPLICATION NUMBER: US 60/168,139
 ; PRIOR FILING DATE: 1999-12-01
 ; NUMBER OF SEQ ID NOS: 13351
 ; SEQ ID NO 11638
 ; LENGTH: 281
 ; TYPE: PRF
 ; ORGANISM: Agrobacterium tumefaciens
 US-09-803-110-11638

Query Match 14.6%; Score 128; DB 22; Length 281;

Best Local Similarity 22.4%; Pred. No. 3.2e-05;
 Matches 58; Conservative 28; Mismatches 89; Indels 84; Gaps 10;

QY 1 MKKALALIALAL-----PAALAE-----ASGFVQAD----- 30
 DB 1 MKKALAGFLAVLTGTSAIADLYQAEPAAYDAPETVTOASGWTLDGDIYSPNKLK 60
 QY 31 AAHAKASSLSGSAKGFSPRI-----SAGYRINDL---REAVDYTRYKNYK----- 72
 DB 61 GAHYGCGPGGYLDPTATIKDSYVIGGVGYQFNPNFRSDVTLIDYMGKSDFRGSTSGF 120
 QY 73 --QVPS-----TDFKLYSIGASATYDDTQSPVKPYTGARL-----SLNRASVDF 115
 DB 121 CGSVPGRCVSADLSLSAYTLMANAYVDLTGYGSIPTPYVGSGIGSYKWDKLRNTSCSV 180
 QY 116 NGSDSFQSTSTG-----LGLVAGSYAVTPNVDLDAGYRYNYIGKVNTY----- 159
 DB 181 NGLCGDPPTTEHGGKGRKRAIYALMAGASIDVTCNLKADIGYFRHINKGDMFAYENGCGP 240
 QY 160 ---KNVRSGLSAGRYVKF 175
 DB 241 GRDKGLYSHEVRVGRYVF 259

RESULT 11
 US-09-489-039A-13699

; Sequence 13699, Application US/09489039A
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; PRIOR FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 13699
 ; LENGTH: 187
 ; TYPE: PRF
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-13699

Query Match 13.3%; Score 116; DB 18; Length 187;
 Best Local Similarity 26.1%; Pred. No. 0.00039;
 Matches 53; Conservative 25; Mismatches 77; Indels 48; Gaps 7;

QY 1 MKKALALIALAL-----PAALAE-----ASGFVQAD----- 44
 DB 5 MKSIARKKVAATIALGASSAACAVNLHGEAGAEFTNLSASFGEPMFTSSQMAHSDN 64
 QY 45 -GFSPRISAGYRINDLREAVDYTRYKNYKQVSTDFKLYSIGASAIY---DPTQSPVK 99
 DB 65 DGDVSGLGMGYNFNLGPF-----LMTLGGKAVYLNKRKDGDEGATA 105
 QY 100 PYLGARLSLNRAVDENGSDSFQSTSTGLV-----LAGSYAVTPNVDLDAGRY-NT 152
 DB 106 AGGGAELPLGGYFTLF-GEGYISPDSSSGYEDVEANAGYRLNVRSLNIEAGYRIDM 164
 QY 153 IGKYNVYKAVNSGELSAGRYVKF 175
 DB 165 AGKDNRNLDLADGAYGVNFRF 187

RESULT 12
 US-09-540-236-2245

; Sequence 2245, Application US/09540236
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CA
 ; FILE REFERENCE: 2709.2005-001
 ; CURRENT APPLICATION NUMBER: US/09/540,236

Search completed: October 28, 2002, 16:11:22

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 28, 2002, 16:01:19 ; Search time 35.9039 Seconds

(without alignments)
1465.185 Million cell updates/sec

Title: US-09-684-883-4

Perfect score: 874
Sequence: 1 MKKALALALALPAALAE.....VTFKNSGSLAGVRKF 175

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 1112697 segs, 300604653 residues

Total number of hits satisfying chosen parameters: 1112697

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/paa/PCF_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/PCF_NEW_COMB.pep1.*
3: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep1.*
6: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep1.*
8: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep1.*
10: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
11: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep1.*
12: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	874	100.0	175	US-09-684-883-4	Sequence 4, Appl
2	843	96.5	175	US-09-684-883-30	Sequence 30, Appl
3	838.5	95.9	174	US-09-684-883-6	Sequence 6, Appl
4	824.5	94.3	174	US-09-684-883-2	Sequence 2, Appl
5	813.5	93.1	174	US-09-684-883-8	Sequence 8, Appl
6	813.5	93.1	25	US-09-684-883-26	Sequence 26, Appl
7	93.5	10.7	353	US-10-203-942-9	Sequence 9, Appl
8	93.5	10.7	369	US-09-545-199F-153	Sequence 153, App
9	89.5	10.2	500	US-09-990-004A-149	Sequence 149, App
10	89.5	10.2	500	US-10-219-220-149	Sequence 149, App
11	87.5	10.0	229	US-10-219-989-9669	Sequence 35699, A
12	86.5	9.9	213	US-09-791-537-112202	Sequence 112202, A
13	86.5	9.9	431	US-09-540-209B-7041	Sequence 7041, Ap
14	86.5	9.9	501	US-09-540-209B-7077	Sequence 7077, Ap
15	86	9.8	332	US-10-193-002-53	Sequence 53, Appl
16	86	9.8	364	US-09-545-199F-151	Sequence 151, App
17	86	9.8	652	US-10-193-002-250	Sequence 350, App
18	86	9.8	765	US-09-791-537-22674	Sequence 22674, A
19	86	9.8	802	US-10-193-002-209	Sequence 209, App
20	86	9.8	802	US-10-193-002-346	Sequence 346, App

21	85.5	9.8	490	US-09-791-537-119822	Sequence 119822, A
22	85	9.7	334	US-10-206-576-106	Sequence 106, App
23	85	9.7	471	US-09-791-537-52271	Sequence 52271, A
24	83	9.5	396	US-10-179-131-9383	Sequence 9383, Ap
25	83	9.5	634	US-09-791-537-9868	Sequence 5868, A
26	83	9.5	634	US-09-791-537-99400	Sequence 99400, A
27	82.5	9.5	634	US-09-791-537-99401	Sequence 99401, A
28	82.5	9.4	187	US-10-219-999-45753	Sequence 45753, A
29	82.5	9.4	228	US-09-791-537-67314	Sequence 67314, A
30	82	9.4	243	US-10-053-853A-1674	Sequence 1674, Ap
31	81	9.3	15	US-09-684-883-23	Sequence 23, Appl
32	81	9.3	641	US-10-108-605-61	Sequence 61, Appl
33	80.5	9.2	421	PCT-US02-12532-123	Sequence 123, App
34	80	9.2	581	US-09-513-996A-64105	Sequence 64105, A
35	80	9.2	645	US-09-513-996A-64105	Sequence 64105, A
36	79.5	9.1	390	US-09-791-537-89799	Sequence 89799, A
37	79.5	9.1	433	US-09-791-537-118678	Sequence 118678, A
38	79.5	9.1	527	US-09-791-537-108323	Sequence 108323, A
39	79.5	9.1	2214	US-60-360-039-22147	Sequence 22147, A
40	79	9.0	15	US-09-684-883-18	Sequence 18, Appl
41	79	9.0	294	US-09-513-996A-13642	Sequence 13642, A
42	79	9.0	294	US-09-513-996A-58290	Sequence 58290, A
43	79	9.0	339	US-09-513-996A-67258	Sequence 67258, A
44	79	9.0	385	US-09-513-996A-13641	Sequence 13641, A
45	79	9.0	385	US-09-513-996A-58289	Sequence 58289, A

ALIGNMENTS

RESULT 1
US-09-684-883-4
Sequence 4, Application US/09684883
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Martlin, Denis
Hamel, Josée
Roux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-684-883-4

Query Match 100.0%; Score 874; DB 9; Length 175;
Best Local Similarity 100.0%; Pred. No. 9, 1e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAALALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNTKQVPSDFKLYSGASAIYDPDQSPVKKPYLGARLSLNRAVDVFNSSDS 120
DB 61 FAVDYTRYKNTKQVPSDFKLYSGASAIYDPDQSPVKKPYLGARLSLNRAVDVFNSSDS 120
QY 121 FSGTSGVLGVLGVSAYATPNVDLAGRYNYIGKVTNVRKNSGELSGAGYRVKF 175
DB 121 FSGTSGVLGVLGVSAYATPNVDLAGRYNYIGKVTNVRKNSGELSGAGYRVKF 175

RESULT 2

US-09-684-883-30
Sequence 30, Application US/09684883

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

Marlin, Denis

Hamel, Josee

Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN

OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/684,883

FILING DATE: 06-Oct-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 175 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 30:

US-09-684-883-30

Query Match 96.5%; Score 843; DB 9; Length 175;
Best Local Similarity 96.6%; Pred. No. 1, 7e-80;
Matches 169; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAALALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNTKQVPSDFKLYSGASAIYDPDQSPVKKPYLGARLSLNRAVDVFNSSDS 120
DB 61 FAVDYTRYKNTKQVPSDFKLYSGASAIYDPDQSPVKKPYLGARLSLNRAVDVFNSSDS 120
QY 121 FSGTSGVLGVLGVSAYATPNVDLAGRYNYIGKVTNVRKNSGELSGAGYRVKF 175
DB 121 FSGTSGVLGVLGVSAYATPNVDLAGRYNYIGKVTNVRKNSGELSGAGYRVKF 175

RESULT 3

US-09-684-883-6
Sequence 6, Application US/09684883

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

Marlin, Denis

Hamel, Josee

Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN

OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/684,883

FILING DATE: 06-Oct-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-684-883-6

Query Match 95.9%; Score 838.5; DB 9; Length 174;

Best Local Similarity 97.1%; Pred. No. 4, 9e-80;

Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 MKKALALIALALPAALAEASGFTYOADAAHAKSSSLGAKGFSPIASGRINDLR 60
Db 1 MKKALATLIALALPAALAEASGFTYOADAAHAKSSSLGAKGFSPIASGRINDLR 60
QY 61 FAVDTYRYKNYKOVSTDFKLYSGASAIYDFPTGQSPVRYGARSLSNRAQSPNGSDS 120
||||| ||||||| ||||||| ||||||| ||||

Db	61	FAVDDYTRKRNK - APSDEFKYSIGASVIVDFDTQSPVAPKPYFGARLSLNRAASHLGSDS	11	19
Qy	121	FSQSTGTGVLAVGASYAVTPVDDADGYRKNYIGKNTWKNNRSGELSLAGRAVFK	175	
Db	120	FKRTSAGIGVLAVGYAVTPVDDADGATRYNVGKNTWKNNRSGELSLAGRAVFK	174	

```

RESULT 6
US-09-684-883-26
; Sequence 26, Application US/09684883
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
;           Martin, Denis
;           Hamel, Josée
;           Rioux, Clement
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/684,883
; FILING DATE: 06-Oct-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 04/998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: 608B
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-684-883-26

Query Match      13.6%; Score 118.5; DB 9; Length 25;
Best Local Similarity 92.3%; Pred. No. 1.9e-05;
Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 1

Oy      61  FAVDYTRYKNYKOVSPDFKLISGA 86
Db      1  PAVDYTRYKNK-APSTDKFLISGA 25

RESULT 7
US-10-203-942-9
; Sequence 9, Application US/10203942
; GENERAL INFORMATION:
; APPLICANT: BERTHET, FRANCOIS-XAVIER
; APPLICANT: DEBOEL, PHILIPPE
; APPLICANT: POOLMAN, JAN
; APPLICANT: THONNARD, JOELLE
; TITLE OF INVENTION: HAEMOPHILUS INFLUENZA OUTER MEMBRANE
; TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION

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      / FILE REFERENCE: B45210
      / CURRENT APPLICATION NUMBER: US/10/203,942
      / CURRENT FILING DATE: 2002-08-15
      / PRIOR APPLICATION NUMBER: PCT/EP01/01556
      / PRIOR FILING DATE: 2001-02-13
      / PRIOR APPLICATION NUMBER: GB 0003502.2
      / PRIOR FILING DATE: 2000-02-15
      / NUMBER OF SEQ ID NOS: 9
      / SOFTWARE: FastSeq for Windows Version 4.0
      / SEQ ID NO 9
      / LENGTH: 353
      / TYPE: PRF
      / ORGANISM: Haemophilus influenzae
      / US-10-203-942-9

Query Match          10.7%; Score 93.5; DB 11; Length 353;
Best Local Similarity 24.9%; Pred. No. 0.27;
Matches    54; Conservative   29; Mismatches    89; Indels    45; Gaps    10;

OY       1 MKKLAALIALPALAALAEGA---SGFYQADAAHAKASSLSGS-----AKGS 47
           ||| ||| : |::||: | : | | | | | | | | | | | | | | | | |
Db        1 MKKTALILVVAAGAAASVQAAPQENTREYAGVKGAQSFDHGJLALREXKVGHNNSTP 60
OY       48 PRISAGRI---NDLFAY----DYTRRYKNYKQVPSTDFKLYSIGA--SAIVDPQTGP 97
           ||| : | | | | | | | | | | | | | | | | | | | | | | | |
Db        61 YGPFGGYQIILNQNLLAVELGYDDFGRAKG-RKGTKVYKHTNHGHLISLKSYEVLG 119
OY       98 VKPYLAGRLSNRASVDENGSDSFSQTSITGLG-----VLAGSVATPTDVIDAG 147
           : | : | : | : | : | : | | | | | | | | | | | | | | | |
Db       120 LDVYGKAGVALVRS--DYKLYNENSTLTAKKCEHHRARASGLFAVGAEYAVLPDLARLE 177
OY       148 Y-----RNYTIGKYNTKYNRS--GELTSAGVRKF 175
           | | | | | | | | | | | | | | | | | | | | | | | |
Db       178 YQLTVRGKTRPODKRFITALNTNPWIGSLNGISTYRF 214
           | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
US-09-545-199F-153
Sequence 153, Application US/09545199F
GENERAL INFORMATION:
APPLICANT: Lowery E., David
APPLICANT: Fuller E., Troy
APPLICANT: Kennedy J., Michael
TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
FILE REFERENCE: 28341/6227.NCP
CURRENT APPLICATION NUMBER: US/09/545,199F
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/153,453
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/128,689
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 153
LENGTH: 369
TYPE: PRF
ORGANISM: Actinobacillus pleuropneumoniae
US-09-545-199F-153

Query Match          10.7%; Score 93.5; DB 9; Length 369;
Best Local Similarity 23.2%; Pred. No. 0.26;
Matches    54; Conservative   34; Mismatches    78; Indels    67; Caps    12;

OY       1 MKKLAALIALPALAALAEGA---SGFYQADAAHAKASSLSGSAR-GPSPRI---SAG 53
           ||| ||| : |::||: | : | | | | | | | | | | | | | | | | |
Db        1 MKSLVALVALYS--AAAVQAAPQONTPEYFAGAKKVGQSSFHNGVQLNSGHDRINDKTR 58
OY       54 YRINDLRPAVDYTRYKNYKQVPSTDFKLYSIGASAIYTF-----DT 94
           ||| : | | | | | : | : | | | | | | | | | | | | | |
Db        59 YGIN--RNSYTGVFEGGYQIILNQN---GLAAELGYDYGRVGNVDERTVKHSAGL 113
OY       95 QSPKPR-----YLGARSLINASVDYFNFGSDSFSQTSNGLCYL-----AGSVTA 137
           : || | | | | | | | | | | | | | | | | | | | | | |

```

D_b 114 NLALKEPEVEPLDDVYGKGVIAVVRNDYKKCKAGCNTNESTTFKHAKASTIIGAGEYE_A 173
Q_Y 138 VTPNDDLACGRNYIKGVNTVKH--VRSG-----ELSKGVYKF 175
 :
 :
 :
D_b 174 ILP--ELAAAREYGYLTKAGLNLALVRSGVDYDFQAPDIHSYVAGLSYRF 224
 :
 :
 :

```

RESULT 9
US-09-990-004A-149
: Sequence 149, Application US/09990004A
: GENERAL INFORMATION:
: APPLICANT: Flihn, Barry
: APPLICANT: Lasham, Annette
: TITLE OF INVENTION: Methods for Modulating Cellular Development and Programmed Cell D
: FILE REFERENCE: 11000.1038c1
: CURRENT APPLICATION NUMBER: US/09/990,004A
: CURRENT FILING DATE: 2002-04-08
: PRIOR APPLICATION NUMBER: US 09/327,373
: PRIOR FILING DATE: 1999-06-04
: NUMBER OF SEQ ID NOS: 204
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 149
: LENGTH: 500
: TYPE: PR1
: ORGANISM: Eucalyptus grandis
: US-09-990-004A-149

```

Query Match	10.2%;	Score 89.5;	DB 9;	Length 500;
Best Local Similarity	22.1%;	Pred. No. 1.1;		
Matches 40;	Conservative 20;	Mismatches 74;	Indels 47;	Gaps 3;

[illegible]

QY	161	N	161
Db	188	D	188

```

RESULT 10
US-10-219-220-149
Sequence 149 Application US/10219220
GENERAL INFORMATION:
APPLICANT: Film, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
FILE REFERENCE: 11000.1022c1
CURRENT APPLICATION NUMBER: US/10/219.220
PRIOR FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. 09/325,932
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 149
LENGTH: 500
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-10-219-220-149

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Query Match	10.2%;	Score 89.5;	DB 11;	Length 500;
Best Local Similarity	22.1%;	Pred. No. 1.1;		
Matches 40;	Conservative 20;	Mismatches 74;	Indels 47;	Gaps 3;

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Oy  4 ALAAALIALALPAALAAEGASFEYQAADAAAHKASSISLGAKGEFPRISACTRI----- 56
Db  32 AAAVAVLALALALTTIASLDMHSIYSYDRAHGDNRSSSSSSSRSDDEWMAVYESWLANHGK  91
Oy  57 -----NDLRFADVTRYKKNKYQVPSYDFKLKYSIGASAIYDFEQSPVK 100
Db  92 AYNALGEEKRFPYQFKDMLRFTIDHN-----AGGDRIYVGLNQFADLNEEYRSM 142
Oy  101 YLGARLSINRASVDENGSDSFQSTGTGLAGVSYAVTPENVDLDAGYRNYTIGKVTYK 160
Db  143 YLGRAM-----DRSGRRIGRARSDRYAVAAEGEELPASVDWRKEGAAVYDK 187
Oy  161 N 161
Db  188 D 188

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QY	161 N 161
Db	188 D 188

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US-10-219-999
RESULT 11
US-10-219-999-59699
Sequence: 59699, Application US/10219999
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 59699
LENGTH: 229
TYPE: PRT
ORGANISM: Zea mays
US-10-219-999-59699

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Query Match	10.0%;	Score 87.5;	DB 11;	Length 229;
Best Local Similarity	28.7%;	Pred. No. 0.65;		
Matches	45;	Conservative	14;	Mismatches 53; Indels 45; Gaps 5;

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0Y      4 ALAALLALPAAALAEASGFTYQADAAHAKKASSLSGSKGFPSTAGYTRINDLRFAY 63
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      82 AAATLVSAAISGSAASTGAAAAASVSAAGAAASGASISGASVGSASATAS----- 131
0Y      64 DYRRKNTYQVPSDTPFKLISGASAIYDFTQSGVVRPYLGARLSLRASY--DENSGDS 122
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      132 -----ASTSTSLDSVSASA---DTGS-----LAATTSVSAGAAVSSFGVSTA 171
0Y      121 FS-----QTSTGLGVLAGVSAVTPPNVD 145
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      172 ASMAASTPAAAAAAASSTGAAVAGTWISTTAIGAVID 208

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RESULT 12
US-09-791-537-112202
; Sequence 112202, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0

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TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-193-002-53

Query Match 9.8%; Score 86; DB 11; Length 332;
Best Local Similarity 27.9%; Pred. No. 1.5;
Matches 43; Conservative 15; Mismatches 60; Indels 36; Gaps 7;

QY 10 ALALPAAALAEAGSGFYVOADAAHAKASSSLGSA-----KGFSPRISAGYRINDLRFA 62
DB 128 SFALPAG-----WVESDAHFDDYGSALSKTTGDPFFPGQPPYVA-----NDTRIV 173
QY 63 VDYTRKKNYKQVPSDFKLYSIGSAIYDFTQSPVKKPYLGARLSLNRAVDENGSD--- 119
DB 174 LGRLDOKLYASAFAATDSK-----AAARLGSDDGFEFMPYPGTRINQETVSLDANGVSGSA 228
QY 120 -----SFQSTSTGLG-VLAGVSYAVTPNVLDAG 147
DB 229 SYEYKFFSDPSKPNQIWTGVIGSPANNAP-DAG 261

Search completed: October 28, 2002, 16:13:51
Job time : 37.9039 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 28, 2002, 16:00:44 ; Search time 103.601 Seconds

(without alignments)
591.158 Million cell updates/sec

Title: US-09-684-883-6

Sequence: 1 MKKALATLIALALPAALAE.....VNTVKNVNSGLSAGRVK 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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22: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
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26: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	854	98.4	174	8	US-08-406-362-2
2	854	98.4	174	22	US-09-479-759-36
3	135	15.6	170	8	US-08-479-520-20
4	135	15.6	170	8	US-08-486-050-20
5	135	15.6	170	8	US-08-486-050A-20
6	135	15.6	170	13	US-08-988-444-20
7	135	15.6	170	16	US-09-217-849-20

8	135	15.6	170	18	US-09-489-850-20	Sequence 20, Appl1
9	130.5	15.0	281	21	US-09-739-449-11638	Sequence 11638, A
10	130.5	15.0	281	22	US-09-803-110-11638	Sequence 11638, A
11	115.5	13.3	187	18	US-09-489-039A-13699	Sequence 13699, A
12	114.5	13.3	198	19	US-09-540-236-2245	Sequence 2245, Ap
13	106.5	12.3	384	19	US-09-543-681A-7922	Sequence 7922, Ap
14	102	11.8	217	16	US-09-252-691C-9162	Sequence 9162, Ap
15	102	11.8	217	16	US-09-252-691C-9162	Sequence 9162, Ap
16	101	11.6	21	26	US-10-082-014-123	Sequence 123, App
17	101	11.6	21	26	US-10-082-014-123	Sequence 123, App
18	97	11.2	21	26	US-10-082-014-124	Sequence 124, App
19	97	11.2	21	26	US-10-082-014-124	Sequence 124, App
20	96	11.1	212	22	PCT-US02-03987-10149	Sequence 10149, A
21	96	11.1	212	22	US-09-815-242-10149	Sequence 10149, A
22	96	11.1	212	24	US-10-072-851-10149	Sequence 5331, Ap
23	95.5	11.0	487	17	US-09-328-352-5331	Sequence 7684, Ap
24	94	10.8	190	19	US-09-543-681A-7684	Sequence 19759, A
25	93.5	10.8	261	16	US-09-252-991A-19759	Sequence 2, Appl1
26	93	10.7	359	4	US-08-065-442-2	Sequence 2, Appl1
27	93	10.7	359	8	US-08-457-997-2	Sequence 2, Appl1
28	93	10.7	359	8	US-08-457-997-2	Sequence 2, Appl1
29	93	10.7	359	8	US-08-457-997-2	Sequence 2, Appl1
30	93	10.7	359	18	US-09-451-184-2	Sequence 2, Appl1
31	92	10.6	257	1	PCT-US02-03987-13845	Sequence 13845, A
32	92	10.6	257	22	US-09-815-242-13845	Sequence 13845, A
33	92	10.6	257	24	US-10-072-851-13845	Sequence 5, Appl1
34	92	10.6	568	7	US-08-331-393-5	Sequence 7451, Ap
35	90.5	10.4	385	18	US-09-902-540-16267	Sequence 16267, A
36	90	10.4	397	23	US-09-328-352-5146	Sequence 5146, Ap
37	90	10.4	643	17	US-09-545-199C-153	Sequence 13821, A
38	89	10.3	225	24	US-09-545-199C-153	Sequence 153, App
39	89	10.3	369	19	US-09-545-199C-153	Sequence 153, App
40	89	10.3	369	22	US-09-809-665A-153	Sequence 9372, Ap
41	89	10.3	369	22	US-09-739-449-9372	Sequence 9372, Ap
42	88.5	10.2	178	21	US-09-803-110-9372	Sequence 8555, Ap
43	88.5	10.2	178	22	US-09-739-449-8555	Sequence 8555, Ap
44	87.5	10.1	213	21	US-09-803-110-8555	Sequence 8555, Ap
45	87.5	10.1	213	22	US-09-803-110-8555	Sequence 8555, Ap

ALIGNMENTS

RESULT 1
US-08-406-362-2
Sequence 2, Application US/08406362
GENERAL INFORMATION:
APPLICANT: Biodeur, Bernard R
APPLICANT: Martini, Denis
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
zip: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,362
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Pharma-43

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-406-362-2

Query Match          98.4%; Score 854; DB 8; Length 174;
Best Local Similarity 98.3%; Pred. No. 3.9e-88;
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALTLIALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
    |||
DB 1 MKKALTLIALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKRYKAPSTDFKLYSGASAIYDPTQSPVKRYLGARLSLNASVDLGSDSF 120
    |||
DB 61 FAVDYTRYKRYKAPSTDFKLYSGASAIYDPTQSPVKRYLGARLSLNASVDLGSDSF 120
QY 121 SQTSLGLVLAGVYAVTPNVDLDAGYRNYIGKVTYKRVNSGELSGVRYKVF 174
    |||
DB 121 SQTSLGLVLAGVYAVTPNVDLDAGYRNYIGKVTYKRVNSGELSGVRYKVF 174

; RESULT 2
; US-09-870-759-36
; Sequence 36, Application US/09870759
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-09-870-759-36

Query Match          98.4%; Score 854; DB 22; Length 174;
Best Local Similarity 98.3%; Pred. No. 3.9e-88;
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALTLIALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
    |||
DB 1 MKKALTLIALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKRYKAPSTDFKLYSGASAIYDPTQSPVKRYLGARLSLNASVDLGSDSF 120
    |||
DB 61 FAVDYTRYKRYKAPSTDFKLYSGASAIYDPTQSPVKRYLGARLSLNASVDLGSDSF 120
QY 121 SQTSLGLVLAGVYAVTPNVDLDAGYRNYIGKVTYKRVNSGELSGVRYKVF 174
    |||
DB 121 SQTSLGLVLAGVYAVTPNVDLDAGYRNYIGKVTYKRVNSGELSGVRYKVF 174

; RESULT 3
; US-08-479-520-20
; Sequence 20, Application US/08479520
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREO, AND USES THEREOF

```

```

; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,520
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/105/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-479-520-20

Query Match          15.6%; Score 135; DB 8; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.6e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLIALPAALAEAGSGFYVQADAAH-----AKASSLSG-----AKG 45
    |||
DB 15 SLLFSSAAQAASEDRSPYVQADLAYAERITHDYPOATGANNTSTVDYFRNRAHS 74
QY 46 FSPRISAGYRINDLRFAVDYTRYKRYN-----KAPSTDFK 79
    |||
DB 75 IHPRVSVGVDGGRIRIADYASYRKMNKNKYSVTKELKNNKKDKLTQNGFTFHA 134
QY 80 LYSTGASAIYDPTQSPVKRYLGARLSLN--RASVD 113
    |||
DB 135 ASSLGLSAIYDFKLGKFKPYIGARVAVGAVRHSID 170

; RESULT 4
; US-08-486-050-20
; Sequence 20, Application US/08486050
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREO, AND USES THEREOF
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-486-050-20

Query Match 15.6%; Score 135; DB 8; Length 170;
Best Local Similarity 26.3%; Pred. NO. 1.6e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATTLALPMAALAGASGYVQADAAH-----AKSSSLGS-----AKG 45
DB 15 SLLFSSAAQAASEDRSPYVQADLVAERITHDYPOATGANNSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFVADYTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDEFGWRIADYASYRKNNKYSVNTKELENKNNKDKLTENGNGTFHA 134
QY 80 LYSIGASAIYDPQSPVYPYLGARSLN--RASVD 113
DB 135 ASSLGSAIYDFKLGKFKPYIGARVAGVHRSID 170

RESULT 5
US-08-486-050A-20
Sequence 20, Application US/08486050A
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-486-050A-20

Query Match 15.6%; Score 135; DB 8; Length 170;
Best Local Similarity 26.3%; Pred. NO. 1.6e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATTLALPMAALAGASGYVQADAAH-----AKSSSLGS-----AKG 45
DB 15 SLLFSSAAQAASEDRSPYVQADLVAERITHDYPOATGANNSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFVADYTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDEFGWRIADYASYRKNNKYSVNTKELENKNNKDKLTENGNGTFHA 134
QY 80 LYSIGASAIYDPQSPVYPYLGARSLN--RASVD 113
DB 135 ASSLGSAIYDFKLGKFKPYIGARVAGVHRSID 170

RESULT 6
US-08-988-444-20
Sequence 20, Application US/08988444
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,444
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,050
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-988-444-20

Query Match 15.6%; Score 135; DB 13; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.6e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLIALPAAALAGASGFYQADAAH-----AKASSSLGS-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYVQADLAFAERITHDYPOATGANNSTVSDYFNRIRAS 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KAPSTDFK 79
DB 75 IHRVSVGYDGGWRIADYASYRKNNNNKYSVTKELENNKNNKDKLTENGNGTFHA 134
QY 80 LYSIGASAIYDPTQSPYKPYLGARSLN--RASVD 113
DB 135 ASSLGSAIYDFKFKGKFPYIGARVAYGVHRHSID 170

RESULT 7

US-09-217-849-20
Sequence 20, Application US/09217849
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,849
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
STRANDEDNESS: <unknown>
TOPOLOGY: unknown
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-09-217-849-20

Query Match 15.6%; Score 135; DB 16; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.6e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLIALPAAALAGASGFYQADAAH-----AKASSSLGS-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYVQADLAFAERITHDYPOATGANNSTVSDYFNRIRAS 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KAPSTDFK 79
DB 75 IHRVSVGYDGGWRIADYASYRKNNNNKYSVTKELENNKNNKDKLTENGNGTFHA 134
QY 80 LYSIGASAIYDPTQSPYKPYLGARSLN--RASVD 113
DB 135 ASSLGSAIYDFKFKGKFPYIGARVAYGVHRHSID 170

RESULT 8

US-09-489-850-20
Sequence 20, Application US/09489850
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/489,850
FILING DATE: 24-Jan-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/988,444
FILING DATE: <unknown>
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
STRANDEDNESS: <unknown>
TOPOLOGY: unknown
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-489-850-20

Query Match 15.6%; Score 135; DB 18; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.6e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLIALPAAALAGASGFYQADAAH-----AKASSSLGS-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYVQADLAFAERITHDYPOATGANNSTVSDYFNRIRAS 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KAPSTDFK 79
DB 75 IHRVSVGYDGGWRIADYASYRKNNNNKYSVTKELENNKNNKDKLTENGNGTFHA 134

QY 80 LVSIGASAIYDPDTPQSPVKPYLGARLSLN--RASVD 113
 Db 135 ASSLGSLAITDFELKKGKRPYIGARVAYGVHRHSID 170

RESULT 9
 US-09-739-449-11638

; Sequence 11638, Application US/09739449
 ; GENERAL INFORMATION:
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15490)C
 ; CURRENT APPLICATION NUMBER: US/09/739,449
 ; CURRENT FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: US 09/514,000
 ; PRIOR FILING DATE: 2000-02-23
 ; NUMBER OF SEQ ID NOS: 13351
 ; SEQ ID NO 11638
 ; LENGTH: 281
 ; TYPE: PRF
 ; ORGANISM: Agrobacterium tumefaciens
 US-09-739-449-11638

Query Match 15.0%; Score 130.5; DB 21; Length 281;
 Best Local Similarity 22.4%; Pred. No. 1.1e-05;
 Matches 60; Conservative 29; Mismatches 76; Indels 103; Gaps 11;

QY 1 MKKALATLIALA-----PAAALAE-----ASGFYQAD----- 30
 Db 1 MKKALAGFLAVLLTGSAIADLYQAEPAAPAVYVYQASGMYLRGDVGSFNKLR 60
 QY 31 AAHAKASSLSGAKGFSPRI-----SAGYRINDL--REAVDYTRKNYKAPSTDF 78
 Db 61 GAHYTGGGPGGYLDGDFDTATIKDSYVIGGVGYQFNNTFRSDVTLIDYMGKSDFRGSTSGF 120
 QY 79 -----KLYSIGASAIYDPDTPQSPVKPYLGARLSLNRAVSVDLGS-----D 118
 Db 121 CGSVGRCSADLSLSATYTMANAYVDLGYGSIPTPYG-----GIGGSYKWD 171
 QY 119 SFSQTS--TGLG-----VLGVSYAVTPPNVDLDAGRYRNTYKQVNT 157
 Db 172 KLRNTSCSVNGLGCDPTTEHGKGMKRPAYALMAGASIDVTCNLKADIGYRFRHINKDM 231
 QY 158 V-----KNVRSGLSAGYRVKF 174
 Db 232 FAYENGCGPRDKGLYSHEVRVGGRYVF 259

RESULT 10

US-09-803-110-11638
 ; Sequence 11638, Application US/09803110
 ; GENERAL INFORMATION:
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15490)D
 ; CURRENT APPLICATION NUMBER: US/09/803,110
 ; CURRENT FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 09/739,449
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: US 09/514,000
 ; PRIOR FILING DATE: 2000-02-23
 ; PRIOR APPLICATION NUMBER: US 60/168,139
 ; PRIOR FILING DATE: 1999-12-01
 ; NUMBER OF SEQ ID NOS: 13351
 ; SEQ ID NO 11638
 ; LENGTH: 281
 ; TYPE: PRF
 ; ORGANISM: Agrobacterium tumefaciens
 US-09-803-110-11638

Query Match 15.0%; Score 130.5; DB 22; Length 281;

Best Local Similarity 22.4%; Pred. No. 1.1e-05;
 Matches 60; Conservative 29; Mismatches 76; Indels 103; Gaps 11;

QY 1 MKKALATLIALA-----PAAALAE-----ASGFYQAD----- 30
 Db 1 MKKALAGFLAVLLTGSAIADLYQAEPAAPAVYVYQASGMYLRGDVGSFNKLR 60
 QY 31 AAHAKASSLSGAKGFSPRI-----SAGYRINDL--REAVDYTRKNYKAPSTDF 78
 Db 61 GAHYTGGGPGGYLDGDFDTATIKDSYVIGGVGYQFNNTFRSDVTLIDYMGKSDFRGSTSGF 120
 QY 79 -----KLYSIGASAIYDPDTPQSPVKPYLGARLSLNRAVSVDLGS-----D 118
 Db 121 CGSVGRCSADLSLSATYTMANAYVDLGYGSIPTPYG-----GIGGSYKWD 171
 QY 119 SFSQTS--TGLG-----VLGVSYAVTPPNVDLDAGRYRNTYKQVNT 157
 Db 172 KLRNTSCSVNGLGCDPTTEHGKGMKRPAYALMAGASIDVTCNLKADIGYRFRHINKDM 231
 QY 158 V-----KNVRSGLSAGYRVKF 174
 Db 232 FAYENGCGPRDKGLYSHEVRVGGRYVF 259

RESULT 11
 US-09-489-039A-13699

; Sequence 13699, Application US/09489039A
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 13699
 ; LENGTH: 187
 ; TYPE: PRF
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-13699

Query Match 13.3%; Score 115.5; DB 18; Length 187;
 Best Local Similarity 26.2%; Pred. No. 0.00031;
 Matches 53; Conservative 25; Mismatches 77; Indels 47; Gaps 7;

QY 1 MKKALATLIALA-----PAAALAE-----ASGFYQAD----- 44
 Db 5 MKSIAKMAVAVVTIALGASSAACAAVNLHGCAEFTNLASFAGBPGMTFSSQMAHSDN 64
 QY 45 -GFSPRISAGYRINDLREAVDYTRKNYKAPSTDFKLYSGASAIY----DFTQSPVKP 99
 Db 65 DGDSVGIAMGYNENLGE-----LMTLGGAAVYILNPKDGEYAI 106
 QY 100 YLGARLSLNRAVSVDLGSDFSQTSSTGLGY-----LAGVSYAVTPPNVDLDAGRY-NTI 152
 Db 107 GGGAELEPLGQ-YFTLEGEYGYSPDSKSSGVEDVEANAGVRLNVRSLNLEAGYRIIDMA 165
 QY 153 GKAVTVNKNVRSGLSAGYRVKF 174
 Db 166 GKDGNDNTLADGAYAGVNERF 187

RESULT 12

US-09-540-236-2245
 ; Sequence 2245, Application US/09540236
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CA
 ; FILE REFERENCE: 2709.2005-001
 ; CURRENT APPLICATION NUMBER: US/09/540,236

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 28, 2002, 16:01:19 ; Search time 35.6987 Seconds

(without alignments)
1465.185 Million cell updates/sec

Title: US-09-684-883-6

Sequence: 1 MKKALATVIALALPAAALAE.....VNTVKNVRSGLSGVRVKE 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1112697 seqs, 300604653 residues

Total number of hits satisfying chosen parameters: 1112697

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Pending_Patents_AA_New:*
2: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
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7: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
9: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
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12: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	868	100.0	174 9 US-09-684-883-6	Sequence 6, Appli
2	854	98.4	174 9 US-09-684-883-2	Sequence 2, Appli
3	847.5	97.6	175 9 US-09-684-883-30	Sequence 3, Appli
4	838.5	96.6	175 9 US-09-684-883-4	Sequence 4, Appli
5	834	96.1	174 9 US-09-684-883-8	Sequence 8, Appli
6	133	15.3	25 9 US-09-684-883-26	Sequence 26, Appli
7	99	11.4	353 11 US-10-203-942-9	Sequence 9, Appli
8	89.5	10.3	339 9 US-09-513-996A-67258	Sequence 67258, A
9	89.5	10.3	534 9 US-09-513-996A-7956	Sequence 7956, A
10	89.5	10.3	765 9 US-09-791-537-22674	Sequence 22674, A
11	89	10.3	229 11 US-10-219-999-59699	Sequence 59699, A
12	89	10.3	369 9 US-09-545-199F-153	Sequence 153, App
13	88	10.1	165 9 US-09-540-209B-7537	Sequence 7537, App
14	87	10.0	16 9 US-09-684-883-15	Sequence 15, Appl
15	87	10.0	500 9 US-09-990-004A-149	Sequence 149, App
16	87	10.0	500 11 US-10-219-999-45753	Sequence 45753, App
17	85	9.8	187 11 US-10-219-999-45753	Sequence 45753, A
18	85	9.8	388 9 US-09-791-537-60560	Sequence 60560, A
19	85	9.8	388 13 US-60-360-039-22903	Sequence 22903, A
20	84	9.7	316 9 US-09-513-996A-67259	Sequence 67259, A

21	84	9.7	364 9 US-09-545-199F-151	Sequence 151, App
22	84	9.7	511 9 US-09-513-996A-7957	Sequence 7957, App
23	84	9.7	511 9 US-09-513-996A-39219	Sequence 39219, A
24	83	9.6	213 9 US-09-791-537-112202	Sequence 112202, A
25	81	9.3	15 9 US-09-684-883-23	Sequence 23, Appl
26	81	9.3	431 9 US-09-540-209B-7041	Sequence 7041, App
27	81	9.3	509 9 US-09-791-537-80797	Sequence 80797, A
28	81	9.3	573 9 US-09-791-537-115703	Sequence 115703, A
29	79.5	9.2	576 9 US-09-540-209B-55271	Sequence 55271, App
30	79.5	9.2	576 9 US-09-791-537-117254	Sequence 117254, App
31	79.5	9.2	581 9 US-09-513-996A-64106	Sequence 64106, A
32	79.5	9.2	645 9 US-09-513-996A-64105	Sequence 64105, A
33	79	9.1	15 9 US-09-684-883-18	Sequence 18, Appl
34	79	9.1	207 9 US-09-570-214B-7	Sequence 7, Appli
35	79	9.1	264 9 US-09-956-508A-4	Sequence 4, Appli
36	79	9.1	273 9 US-09-882-227-80	Sequence 80, Appl
37	79	9.1	421 2 PCT-US02-12532-123	Sequence 123, App
38	79	9.1	427 9 US-09-540-209B-6145	Sequence 6145, App
39	79	9.1	490 9 US-09-791-537-119822	Sequence 119822, A
40	78.5	9.0	153 9 US-09-905-176-22	Sequence 22, Appl
41	78.5	9.0	189 11 US-10-108-260A-3443	Sequence 3443, App
42	78.5	9.0	189 11 US-10-108-260A-3443	Sequence 3443, App
43	78.5	9.0	792 11 US-10-179-131-8424	Sequence 8424, App
44	78.5	9.0	792 11 US-10-179-131-8424	Sequence 2, Appli
45	78	9.0	15 9 US-09-684-883-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-684-883-6
Sequence 6, Application US/09684883
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Martin, Denis
Hamel, Josee
Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-Nov-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-Mar-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-Aug-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-684-883-6

Query Match 100.0%; Score 868; DB 9; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.6e-81;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALBAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALBAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRKNNKAPSTDFPKLSTIGASAIYDPDQSPVKPYLGARLSINRASVDLGSDSF 120
DB 61 FAVDYTRKNNKAPSTDFPKLSTIGASAIYDPDQSPVKPYLGARLSINRASVDLGSDSF 120
QY 121 SQTSTGLVLAGSVAVTPNVDDAGRYRNYIGKNTVKNVRSGLSAGYRVKF 174
DB 121 SQTSTGLVLAGSVAVTPNVDDAGRYRNYIGKNTVKNVRSGLSAGYRVKF 174

RESULT 2

US-09-684-883-2

Sequence 2, Application US/09684883

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

Martin, Denis

Hamel, Josee

Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/684,883

FILING DATE: 06-Oct-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 98.4%; Score 854; DB 9; Length 174;
Best Local Similarity 98.3%; Pred. No. 4.4e-80;
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALBAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALBAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRKNNKAPSTDFPKLSTIGASAIYDPDQSPVKPYLGARLSINRASVDLGSDSF 120
DB 61 FAVDYTRKNNKAPSTDFPKLSTIGASAIYDPDQSPVKPYLGARLSINRASVDLGSDSF 120
QY 121 SQTSTGLVLAGSVAVTPNVDDAGRYRNYIGKNTVKNVRSGLSAGYRVKF 174
DB 121 SQTSTGLVLAGSVAVTPNVDDAGRYRNYIGKNTVKNVRSGLSAGYRVKF 174

RESULT 3

US-09-684-883-30

Sequence 30, Application US/09684883

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

Martin, Denis

Hamel, Josee

Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/684,883

FILING DATE: 06-Oct-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 175 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 30:

US-09-684-883-30

Query Match 97.6%; Score 847.5; DB 9; Length 175;

Best Local Similarity 98.3%; Pred. No. 2.1e-79;

Matches 172; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MKKALATLIALPAALAAEGASGFYVQADAAHAKASSISGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAALAAEGASGFYVQADAAHAKASSISGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKKNYK-APSTDFLYSIGASAIYDFPTQSPVKPYLGARLSLNRAVDLGSSDS 119
DB 61 FAVDYTRYKKNYKAPSTDFLYSIGASAIYDFPTQSPVKPYLGARLSLNRAVDLGSSDS 120
QY 120 FSQSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNVTKNVRSGLSAGYRVKF 174
DB 121 FSQSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNVTKNVRSGLSAGYRVKF 175

RESULT 4
US-09-684-883-4
Sequence 4, Application US/09684883
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Martin, Denis
Hamel, Josee
Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-684-883-4

Query Match 96.6%; Score 838.5; DB 9; Length 175;
Best Local Similarity 97.1%; Pred. No. 1.8e-78;
Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 MKKALATLIALPAALAAEGASGFYVQADAAHAKASSISGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAALAAEGASGFYVQADAAHAKASSISGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKKNYK-APSTDFLYSIGASAIYDFPTQSPVKPYLGARLSLNRAVDLGSSDS 119
DB 61 FAVDYTRYKKNYK-APSTDFLYSIGASAIYDFPTQSPVKPYLGARLSLNRAVDLGSSDS 119

DB 61 FAVDYTRYKKNYKAPSTDFLYSIGASAIYDFPTQSPVKPYLGARLSLNRAVDLGSSDS 120
QY 120 FSQSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNVTKNVRSGLSAGYRVKF 174
DB 121 FSQSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNVTKNVRSGLSAGYRVKF 175

RESULT 5
US-09-684-883-8
Sequence 8, Application US/09684883
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Martin, Denis
Hamel, Josee
Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-684-883-8

Query Match 96.1%; Score 834; DB 9; Length 174;
Best Local Similarity 95.4%; Pred. No. 5.2e-78;
Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAAEGASGFYVQADAAHAKASSISGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAALAAEGASGFYVQADAAHAKASSISGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKKNYKAPSTDFLYSIGASAIYDFPTQSPVKPYLGARLSLNRAVDLGSSDSF 120
DB 61 FAVDYTRYKKNYKAPSTDFLYSIGASAIYDFPTQSPVKPYLGARLSLNRAVDLGSSDSF 120
QY 121 FSQSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNVTKNVRSGLSAGYRVKF 174
DB 121 FSQSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNVTKNVRSGLSAGYRVKF 174

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RESULT 6
US-09-684-883-26
; Sequence 26, Application US/09684883
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; Hamel, Denise
; Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/684,883
; FILING DATE: 06-Oct-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: 608B
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-684-883-26

Query Match 15.3%; Score 133; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.3e-07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61 FAVDYTRYKNKAPSTDFKLXSIGA 85
Db 1 FAVDYTRYKNKAPSTDFKLXSIGA 25

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FILE REFERENCE: B45210
; CURRENT APPLICATION NUMBER: US/10/203,942
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP01/01556
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: GB 0003502.2
; PRIOR FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-203-942-9

Query Match 11.4%; Score 99; DB 11; Length 353;
Best Local Similarity 24.8%; Pred. No. 0.095;
Matches 53; Conservative 29; Mismatches 92; Indels 40; Gaps 9;

OY 1 MKKALATLIALALPAAALAECA--SGFYQAADAHAHAKASSLSGS-----AKGFS 47
Db 1 MKKTAIALVAVGLAASVQAAPQENTFYAGVKAGQASFDGLRALAREYKGYHNSFY 60
OY 48 PRISAGYI---NDLRAY-----DYTRYKNKAPSTDFKLXSIGA--SAIYDFDQSPV 97
Db 61 YGVEGGYQIILQNNILGLAVELGYDDPGRAGREKGVVXHTNTHLSLKGSEVLEGL 120
OY 98 KPYLGARSLNRASVDLGGSDFSQTSSTG-----LGVLA-GVSYAVTPNVDLAGY-- 147
Db 121 DYGAGAGALVRSIDYKLYNENSTLKKLGEHHRARASGLFVAGVAVLELAVRLLEYQW 180
OY 148 ----RNYIYGVNTVKNVRS--GELSGAVRYKF 174
Db 181 LTRVGKYRPQDKPMTALNYPWIGSINAGISYRF 214

RESULT 8
US-09-513-996A-67258
; Sequence 67258, Application US/09513996A
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
; FILE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-709P
; CURRENT APPLICATION NUMBER: US/09/513,996A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 81028
; SEQ ID NO 67258
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 1..339
; OTHER INFORMATION: any n or xaa = unknown
; OTHER INFORMATION: Location 1..339 / Ceres Seq. ID 2177695
US-09-513-996A-67258

Query Match 10.3%; Score 89.5; DB 9; Length 339;
Best Local Similarity 27.7%; Pred. No. 0.87;
Matches 39; Conservative 20; Mismatches 53; Indels 29; Gaps 8;

OY 39 SLGSAKF-----SPRISAGYRINDLRFADV--TRYKNKAPSTDFKLXSIGASAIY 89
Db 18 SFSKAKMFIESPKEVSPVWK--YTENEIHSYVDYETFEVHEKVNQYQWIVPKYVXY 75
OY 90 DEDTQSPYKPYLGARSLNRASVDLGGSDFSQTSSTGVLAA--GVSYAVTPNVDLAG 146
Db 76 DPKTDIRY-PKLGVMV-----VGLGGNNGSTLTA--GVLNKGISWATKDKVQ---- 121
OY 147 RYNYIYGVNTVKNVRSGLS 167

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Query Match      10.3% Score 89.5; DB 9; Length 765;
Best Local Similarity 26.1%; Pred. No. 2.5;
Matches 29; Conservative 20; Mismatches 49; Indels 13; Gaps 4
QY 46 EEPRIASAGRYINDLRFAYDYRTRKKNYPASDFELYSIGASAIYDFTQSPPVKPYLGARL 105
    | | | | | | | | | | | | | : : : : : | : | : |
Db 630 FEPIYI-GARLINLSFALDQT--FWYRNSSLVSL-AGGQINETSRRWNPDLVLGGKL 683
    : : : : : : : : : : : : : : : : : : : : : :
QY 106 SLNRASV-----DLGSDSEFSQSTGTGLAIVSYAVTPNPDLDGTRY 149
    : : : : : : : : : : : : : : : : : : : : : :

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Query Match	10.38;	Score 89;	DB 9;	Length 369;
Best Local Similarity	21.58;	Pred. No. 1.1;		
Matches 49;	Conservative 36;	Mismatches 85;	Indels 58;	Gaps 11.
0Y	1	MKKALATLIALPALPAALAEGA-----	SGPYVADDAHAKKASSLCSAK-GSPR-----	49

DB 1 MKRSIALVALAVLS--AAVAQAAPQONTFFAGAKVGOSSHHVNOCLKSGHNDRYNDKTRK 58
QY 50 -----ISAGYRI--NDLRPAVD--YTRKKNKAPSTDFKLISIGASAIY----- 89
DB 59 YGIRNSVTVYGVGGQIINNONNFGIAMELGIDYGRVANGVDERFVYKSHAGNIALLK 118
QY 90 -DDPDQSPKPKPIGASLISNRASVDLGSDFSPQSTGCVL-----AGSYAVATPNV 141
DB 119 PSTEVLPDIDYTGKGIAYVANDYKRYGAEINNESTTKHKAKASTIIGAGYEYAILP-- 176
QY 142 DLDAGRYNYIGKVTNKN--VRSG-----ELSGAVRYKE 174
DB 177 ELAARVEYQLUNKKAGNLKALVRSGTQVDVQYAPDIHSVTAGLSYRF 224
RESULT 13
US-09-540-209B-7537
; Sequence 7537, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
; FILE REFERENCE: 2709.1001-001
; CURRENT APPLICATION NUMBER: US/09/540,209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7537
; LENGTH: 165
; TYPE: PRN
; ORGANISM: B. fragilis
US-09-540-209B-7537
Query Match 10.1%; Score 88; DB 9; Length 165;
Best Local Similarity 22.8%; Pred. No. 0.48; Indels 30; Gaps 7;
Matches 41; Conservative 30; Mismatches 79; Indels 30; Gaps 7;
QY 1 MKRALTLALALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
DB 6 MKRLIMIVCLLVSVTVQAFKQKWIIVPSV-----TGLGLSYKSEKTOFGLAQOGGA 60
QY 61 FAVD-----YTRKKNKAPSTDFKLISIGASAIYDDTQSPKPKPIGASLISNRASVDLG 115
DB 61 FLVDNALMLTLAGANMSKPEDK---YTLGVGGRYVD---KCGIYLGAGLKNRKNMKVKG 114
QY 116 GSDPFSOTSTGLGVAGSYAVTPNVLDAGYRYNYIGKVNKVRSELSA-GVRYRF 174
DB 115 DTIDFA-----FGAEAGYAFILRTYTIERAVYIDL-----SPKDDLSNFGIAKGF 161
RESULT 14
US-09-684-883-15
; Sequence 15, Application US/09684883
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; Martlin, Denis
; Hamel, Josee
; Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/684,883
; FILING DATE: 06-Oct-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEEX: 904136
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: 608B
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-684-883-15
Query Match 10.0%; Score 87; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61 FAVDTRYKNKAPST 76
DB 1 FAVDTRYKNKAPST 16
RESULT 15
US-09-990-004A-149
; Sequence 149, Application US/09990004A
; GENERAL INFORMATION:
; APPLICANT: Finn, Barry
; TITLE OF INVENTION: Methods for Modulating Cellular Development and Programmed Cell
; FILE REFERENCE: 11000.1038c1
; CURRENT APPLICATION NUMBER: US/09/990,004A
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/327,373
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 149
; LENGTH: 500
; TYPE: PRN
; ORGANISM: Eucalyptus grandis
US-09-990-004A-149
Query Match 10.0%; Score 87; DB 9; Length 500;
Best Local Similarity 23.7%; Pred. No. 2.6;
Matches 41; Conservative 19; Mismatches 81; Indels 32; Gaps 4;
QY 4 ALATLIALALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRI----- 56
DB 32 AAVAVIALALALTTIASALDSIVSYDRAHGRSSSSSSWRSDDEVAVYESWLAKHGK 91
QY 57 -----NDLRPAV--DYTRKKNKAPSTDFKLISIGASAIYDDTQSPKPKPIGASL 107
DB 92 AYNALGEKEKRYQFKMDIRFDIDHNAAGD--RTYVGLNDFADLTNEYSRMYGARR-- 148
QY 108 NNASVDLGSDFSPQSTGGLGVAGSYAVTPNVLDAGYRYNYIGKVNKVRSELSA-- 160

Tue Oct 29 09:23:19 2002

us-09-684-883-6.rapn

Page 7

Db 149 -----DRSGRRIGRARSDRYAVANGCELLPASVDMRKEGAVYVDKD 188

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Job time : 36.6987 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 28, 2002, 16:00:44 ; Search time 103.601 Seconds

(without alignments)
591.158 Million cell updates/sec

Title: US-09-684-883-8

Perfect score: 870
Sequence: 1 MKKALALIALALPAALAE.....VNTYKNSGELSGVRVKE 174Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	825	94.8	174	22	US-09-870-759-36
3	125	14.4	170	8	US-08-479-520-20
4	125	14.4	170	8	US-08-486-050-20
5	125	14.4	170	8	US-08-486-050A-20
6	125	14.4	170	13	US-08-988-444-20
7	125	14.4	170	16	US-09-217-849-20

8	125	14.4	170	18	US-09-489-850-20	Sequence 20, Appl
9	124.5	14.3	281	21	US-09-739-449-11638	Sequence 11638, A
10	124.5	14.3	281	22	US-09-803-110-11638	Sequence 11638, A
11	113.5	13.0	187	18	US-09-489-039A-13699	Sequence 13699, A
12	112.5	12.9	98	19	US-09-540-236-2245	Sequence 2245, Ap
13	107	12.3	217	16	US-09-252-691-9162	Sequence 9162, Ap
14	107	12.3	217	16	US-09-252-691C-9162	Sequence 9162, Ap
15	104	12.0	359	8	US-08-065-442-2	Sequence 2, Appl
16	104	12.0	359	8	US-08-457-997-2	Sequence 2, Appl
17	104	12.0	359	8	US-08-457-997A-2	Sequence 2, Appl
18	104	12.0	359	8	US-08-457-722-2	Sequence 2, Appl
19	104	12.0	359	18	US-09-451-184-2	Sequence 2, Appl
20	101	11.6	21	24	US-10-082-014-123	Sequence 123, Appl
21	101	11.6	21	26	US-09-358-618-47	Sequence 47, Appl
22	97.5	11.2	384	19	US-09-543-681A-7922	Sequence 7922, Ap
23	97	11.1	21	24	US-10-082-014-124	Sequence 124, Ap
24	97	11.1	21	26	US-09-418-980-10	Sequence 48, Appl
25	96	11.0	369	19	US-09-418-980-10	Sequence 10, Appl
26	96	11.0	369	19	US-09-506-078-46	Sequence 46, Appl
27	96	11.0	369	26	US-09-120-454-46	Sequence 46, Appl
28	95.5	11.0	212	1	PCT-US02-03987-10149	Sequence 10149, A
29	95.5	11.0	212	22	US-09-815-242-10149	Sequence 10149, A
30	95.5	11.0	212	24	US-10-072-851-10149	Sequence 10149, A
31	95.5	11.0	487	17	PCT-US02-03987-13845	Sequence 13845, A
32	95	10.9	257	1	PCT-US02-03987-13845	Sequence 13845, A
33	95	10.9	257	22	US-09-815-242-13845	Sequence 13845, A
34	95	10.9	257	24	US-10-072-851-13845	Sequence 13845, A
35	95	10.9	369	19	US-09-545-199C-153	Sequence 153, App
36	95	10.9	369	19	US-09-545-199C-153	Sequence 153, App
37	95	10.9	369	22	US-09-809-665A-153	Sequence 153, App
38	95	10.9	397	23	US-09-902-540-16267	Sequence 16267, A
39	94.5	10.9	799	16	US-09-201-228A-203	Sequence 203, App
40	93	10.7	190	19	US-09-543-681A-7684	Sequence 7684, Ap
41	93	10.6	364	18	US-09-418-980-8	Sequence 8, Appl
42	92	10.6	364	19	US-09-506-078-45	Sequence 45, Appl
43	92	10.6	364	19	US-09-545-199C-151	Sequence 151, App
44	92	10.6	364	19	US-09-545-199D-151	Sequence 151, App
45	92	10.6	364	22	US-09-809-665A-151	Sequence 151, App

ALIGNMENTS

RESULT 1
US-08-406-362-2
; Sequence 2, Application US/08406362
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; Zip: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/406,362
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Pharma-43

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-596-9000
 TELEFAX: 212-596-9090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 174 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-406-362-2

Query Match 94.8%; Score 825; DB 8; Length 174;
 Best Local Similarity 94.3%; Pred. No. 9.7e-85;
 Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKKALALIALPALAALAGAGSYVOADAAHAKASSISGSAKSPRISAGRYINDLR 60
 DB 1 MKKALALIALPALAALAGAGSYVOADAAHAKASSISGSAKSPRISAGRYINDLR 60
 QY 61 FAVDYTRYKNTKAPSTDFKLYSIGASYIDFDTQSPVKPYFGARLSLNRAHAGSDSP 120
 DB 61 FAVDYTRYKNTKAPSTDFKLYSIGASYIDFDTQSPVKPYFGARLSLNRAHAGSDSP 120
 QY 121 SKTSAGIGVLAGSYAVTPNVDLAGRYRYVKNVTYKVRSGELSGARYKVF 174
 DB 121 SKTSAGIGVLAGSYAVTPNVDLAGRYRYVKNVTYKVRSGELSGARYKVF 174

RESULT 2
 US-09-870-759-36
 Sequence 36, Application US/09870759
 GENERAL INFORMATION:
 APPLICANT: TERMAN, David S
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 FILE REFERENCE: 870759
 CURRENT APPLICATION NUMBER: US/09/870,759
 CURRENT FILING DATE: 2002-01-14
 PRIOR APPLICATION NUMBER: US 60/208,128
 PRIOR FILING DATE: 2000-05-30
 NUMBER OF SEQ ID NOS: 166
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 36
 LENGTH: 174
 TYPE: PRT
 ORGANISM: Neisseria meningitidis
 US-09-870-759-36

Query Match 94.8%; Score 825; DB 22; Length 174;
 Best Local Similarity 94.3%; Pred. No. 9.7e-85;
 Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKKALALIALPALAALAGAGSYVOADAAHAKASSISGSAKSPRISAGRYINDLR 60
 DB 1 MKKALALIALPALAALAGAGSYVOADAAHAKASSISGSAKSPRISAGRYINDLR 60
 QY 61 FAVDYTRYKNTKAPSTDFKLYSIGASYIDFDTQSPVKPYFGARLSLNRAHAGSDSP 120
 DB 61 FAVDYTRYKNTKAPSTDFKLYSIGASYIDFDTQSPVKPYFGARLSLNRAHAGSDSP 120
 QY 121 SKTSAGIGVLAGSYAVTPNVDLAGRYRYVKNVTYKVRSGELSGARYKVF 174
 DB 121 SKTSAGIGVLAGSYAVTPNVDLAGRYRYVKNVTYKVRSGELSGARYKVF 174

RESULT 3
 US-08-479-520-20
 Sequence 20, Application US/08479520
 GENERAL INFORMATION:
 APPLICANT: VAN ALSTYNE, Diane
 APPLICANT: SHARMA, Lawrence Rajendra
 TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
 TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
 TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREO, AND USES THEREOF

NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/479,520
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/127,499
 FILING DATE: 28-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 51916/105/INBI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 170 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 US-08-479-520-20

Query Match 14.4%; Score 125; DB 8; Length 170;
 Best Local Similarity 25.2%; Pred. No. 2.4e-05;
 Matches 37; Conservative 18; Mismatches 46; Indels 46; Gaps 3;

QY 6 AALIALALPALAALAGAGSYVOADAAHAKASSISGSAKSPRISAGRYINDLR 60
 DB 15 SLLTSSNAQAASEDRRPFYVOADLAERITHTDYQATGANNSTVSDFRNIAHS 74
 QY 46 FSPRISAGRYINDLRFAVDYTRYKNTYKVRSGELSGARYKVF 79
 DB 75 IHPRVSGYDEFGWRIADYASYSRKNNKYSVNTKELENKHNKKDKLTENQNGTFHA 134
 QY 80 LXSIGASYIDFDTQSPVKPYFGARLS 106
 DB 135 ASLSIGASYIDFDTQSPVKPYFGARVA 161

RESULT 4
 US-08-486-050-20
 Sequence 20, Application US/08486050
 GENERAL INFORMATION:
 APPLICANT: VAN ALSTYNE, Diane
 APPLICANT: SHARMA, Lawrence Rajendra
 TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
 TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
 TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREO, AND USES THEREOF
 NUMBER OF SEQUENCES: 75
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

RESULT 5
 US-08-486-050A
 : Sequence 20, Application US/08486050A
 : GENERAL INFORMATION:
 : APPLICANT: VAN ALSTYNE, Diane
 : APPLICANT: SHARMA, Lawrence Rajendra
 : TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
 : TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
 : TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
 : NUMBER OF SEQUENCES: 75
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Foley & Lardner
 : STREET: 3000 K Street, N.W., Suite 500
 : City: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20007-5109
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/486,050A
 : FILING DATE: 07-JUN-1995
 : CLASSIFICATION: 424
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/127,499
 : FILING DATE: 28-SEP-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: BENT, Stephen A.

RESULT 6
 US-08-988-444-20
 ; Sequence 20, Application US/08988444
 ; GENERAL INFORMATION:
 ; APPLICANT: VAN ALSTYNE, Diane
 ; APPLICANT: SHARMA, Lawrence Rajendra
 ; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
 ; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
 ; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 75
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; City: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/988,444
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/486,050
 ; FILING DATE: 07-JUN-1995
 ; APPLICATION NUMBER: US 08/127,499
 ; FILING DATE: 28-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 51916/103/INBI
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 170 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-988-444-20

Query Match 14.4%: Score 125; DB 13; Length 170;
Best Local Similarity 25.2%: Pred. No. 2.4e-05;
Matches 37; Conservative 18; Mismatches 46; Indels 46; Gaps 3;

QY 6 AALIALPAAALAEAGSGFYVOADAH-----AKASSLSGS-----AKG 45
DB 15 SLLFSSAAQAASEDRSPYVOADLAYAERITHDYPOATGANNSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDFGGMRIADYASYRKNNKYSVNTKELENKNNKDKLTENQENGTFHA 134
QY 80 LYSIGASVYDFDQSPFKPYFGARLS 106
DB 135 ASSIGLSAIDFKKFKPKYIGARVA 161

RESULT 7

US-09-217-849-20
Sequence 20, Application US/09217849
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,849
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-09-217-849-20

Query Match 14.4%: Score 125; DB 16; Length 170;
Best Local Similarity 25.2%: Pred. No. 2.4e-05;
Matches 37; Conservative 18; Mismatches 46; Indels 46; Gaps 3;

QY 6 AALIALPAAALAEAGSGFYVOADAH-----AKASSLSGS-----AKG 45
DB 15 SLLFSSAAQAASEDRSPYVOADLAYAERITHDYPOATGANNSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDFGGMRIADYASYRKNNKYSVNTKELENKNNKDKLTENQENGTFHA 134
QY 80 LYSIGASVYDFDQSPFKPYFGARLS 106
DB 135 ASSIGLSAIDFKKFKPKYIGARVA 161

RESULT 8

US-09-489-850-20
Sequence 20, Application US/09489850
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/489,850
FILING DATE: 24-Jan-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/988,444
FILING DATE: <unknown>
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: unknown
US-09-489-850-20

Query Match 14.4%: Score 125; DB 18; Length 170;
Best Local Similarity 25.2%: Pred. No. 2.4e-05;
Matches 37; Conservative 18; Mismatches 46; Indels 46; Gaps 3;

QY 6 AALIALPAAALAEAGSGFYVOADAH-----AKASSLSGS-----AKG 45
DB 15 SLLFSSAAQAASEDRSPYVOADLAYAERITHDYPOATGANNSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDFGGMRIADYASYRKNNKYSVNTKELENKNNKDKLTENQENGTFHA 134

QY 80 LKSGASVITDFDQSPYKPYFGARLS 106
 DB 135 ASSLSGLSAIYDFLKGKFKPYIGARVA 161

RESULT 9

US-09-739-449-11638
 ; Sequence 11638, Application US/09739449
 ; GENERAL INFORMATION:
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15490)C
 ; CURRENT APPLICATION NUMBER: US/09/739,449
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: US 09/514,000
 ; PRIOR FILING DATE: 2000-02-23
 ; NUMBER OF SEQ ID NOS: 13351
 ; SEQ ID NO 11638
 ; LENGTH: 281
 ; TYPE: PR1
 ; ORGANISM: Agrobacterium tumefaciens
 US-09-739-449-11638

Query Match 14.3%; Score 124.5; DB 21; Length 281;
 Best Local Similarity 21.6%; Pred. No. 5.6e-05;
 Matches 58; Conservative 29; Mismatches 78; Indels 103; Gaps 11;

QY 1 MKKALALIALAL-----PAALAE-----ASGFYVAD----- 30
 DB 1 MKNALAGFLAVLLTGTSAIADLYQAEPAAYVDAPVTVQASGWYLRGDVGSFNKLR 60
 QY 31 AAHAKASSLSGAKGSPRI-----SAGYRINDL---RFVADYTRYKNYKAPSTDF 78
 DB 61 GAHYGGGPGGLQDFDITATIKDSVYIGGVGYQFNNTFRSDVTLDYMGKSDFRGSGTSGF 120
 QY 79 -----KLVSIGASVITDFDQSPYKPYFGARLSINRAHAGCS-----D 118
 DB 121 CGSVPRCVSADLSLSTANTLMANAYVDLGTGYSTIPYV-----GGIGGSYVAKMD 171
 QY 119 SFSKTSIA-----GLG-----VLGVSYAVTPVNDLADAGRYNYVAKVNT 157
 DB 172 KLRTSCSVNGLGCDPTTEHGKGMKMPAYALMAGASIDVTCNLKADIGYRHRHINKGDM 231
 QY 158 V-----KNVSGELSGAVRYKF 174
 DB 232 FAYENGSGPRGDKGLYSHVAVGGRYVF 259

RESULT 10

US-09-803-110-11638
 ; Sequence 11638, Application US/09803110
 ; GENERAL INFORMATION:
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15490)D
 ; CURRENT APPLICATION NUMBER: US/09/803,110
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 09/739,449
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: US 09/514,000
 ; PRIOR FILING DATE: 2000-02-23
 ; PRIOR APPLICATION NUMBER: US 60/168,139
 ; PRIOR FILING DATE: 1999-12-01
 ; NUMBER OF SEQ ID NOS: 13351
 ; SEQ ID NO 11638
 ; LENGTH: 281
 ; TYPE: PR1
 ; ORGANISM: Agrobacterium tumefaciens
 US-09-803-110-11638

Query Match

14.3%; Score 124.5; DB 22; Length 281;

Best Local Similarity 21.6%; Pred. No. 5.6e-05;
 Matches 58; Conservative 29; Mismatches 78; Indels 103; Gaps 11;

QY 1 MKKALALIALAL-----PAALAE-----ASGFYVAD----- 30
 DB 1 MKNALAGFLAVLLTGTSAIADLYQAEPAAYVDAPVTVQASGWYLRGDVGSFNKLR 60
 QY 31 AAHAKASSLSGAKGSPRI-----SAGYRINDL---RFVADYTRYKNYKAPSTDF 78
 DB 61 GAHYGGGPGGLQDFDITATIKDSVYIGGVGYQFNNTFRSDVTLDYMGKSDFRGSGTSGF 120
 QY 79 -----KLVSIGASVITDFDQSPYKPYFGARLSINRAHAGCS-----D 118
 DB 121 CGSVPRCVSADLSLSTANTLMANAYVDLGTGYSTIPYV-----GGIGGSYVAKMD 171
 QY 119 SFSKTSIA-----GLG-----VLGVSYAVTPVNDLADAGRYNYVAKVNT 157
 DB 172 KLRTSCSVNGLGCDPTTEHGKGMKMPAYALMAGASIDVTCNLKADIGYRHRHINKGDM 231
 QY 158 V-----KNVSGELSGAVRYKF 174
 DB 232 FAYENGSGPRGDKGLYSHVAVGGRYVF 259

RESULT 11

US-09-489-039A-13699
 ; Sequence 13699, Application US/09489039A
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; PRIOR FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 13699
 ; LENGTH: 187
 ; TYPE: PR1
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-13699

Query Match 13.0%; Score 113.5; DB 18; Length 187;
 Best Local Similarity 25.7%; Pred. No. 0.00055;
 Matches 52; Conservative 25; Mismatches 78; Indels 47; Gaps 7;

QY 1 MKKALALIALA--LALPAALAEAGSGFYVQDAAHAKASSLSGAK----- 44
 DB 5 MKSIAAKWVAATIALGASSACAANLHGEAGAEFTNLASFGAGBPMTFSSQMAHSDN 64
 QY 45 -GFSPRISAGYRINDLRFVADYTRYKNYKAPSTDFKLYSGASYI---DEDTQSPYK 99
 DB 65 DGDVSGGLMGCTNPNLGP-----LMTLGGKAVYINPKDGGEGVIAA 106
 QY 100 YFGARLSINRAHAGSDSFSKTSAGLV-----LAGVSYAVTPVNDLADAGRY- NYV 152
 DB 107 GGGAELPLGQYFT-LFEGGYSPDSMSSGVEDYEANAGVRLNRPRLNEAGRYIDMA 165
 QY 153 GKVTVMKVRSGELSGAVRYKF 174
 DB 166 GKDGNDRTTLADGAYAGVNRFR 187

RESULT 12

US-09-540-236-2245
 ; Sequence 2245, Application US/09540236
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CA
 ; FILE REFERENCE: 2709.2005-001
 ; CURRENT APPLICATION NUMBER: US/09/540,236

;; CURRENT FILING DATE: 2000-04-04
;; NUMBER OF SEQ ID NOS: 3840
;; SEQ ID NO 2245
;; LENGTH: 98
;; TYPE: PRT
;; ORGANISM: M. catarrhalis
US-09-540-236-2245

Query Match 12.9%; Score 112.5; DB 19; Length 98;
Best Local Similarity 39.7%; Pred. No. 0.00027;
Matches 23; Conservative 12; Mismatches 18; Indels 5; Gaps 2;

QY 122 KTSAGLGLVAGVAVTPVDLAGYRYNVG---KVNTVKVRSGLSAGV---GVRYKF 174
DB 41 ETVAGGCVLAGAQAAYALNPOLSVAGVEYVNLGKYDKLDIAKSKAKAQYAKVGLRHNF 98

RESULT 13
US-09-252-691-9162

;; Sequence 9162, Application US/09252691B
;; GENERAL INFORMATION:
;; APPLICANT: Keith G. Weinstein et al.
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
;; FILE REFERENCE: 107196.135
;; CURRENT APPLICATION NUMBER: US/09/252,691B
;; CURRENT FILING DATE: 1999-02-18
;; NUMBER OF SEQ ID NOS: 11324
;; SEQ ID NO 9162
;; LENGTH: 217
;; TYPE: PRT
;; ORGANISM: Enterobacter cloacae
US-09-252-691-9162

Query Match 12.3%; Score 107; DB 16; Length 217;
Best Local Similarity 22.9%; Pred. No. 0.0037;
Matches 49; Conservative 38; Mismatches 79; Indels 48; Gaps 9;

QY 1 MKK-ALMALIALPAAALAEAGSGFYVQADAAHAKASSISGAKGSPRISAGYRI-ND 58
DB 8 MKLIAVAALLISLSGCAVYAHGAEFFIRAGSAIVRTESDNLGM-----GCFVNSNN 62
QY 59 LRFAYDT-----RYKNKAPSTDV-KLYISGASVY---YDFDTQSPV 97
DB 63 TOLGTFYMATDNGVELLAATPFRRHVGLGPTGDIATVHLPPIIMAOYFGDSSSKV 122
QY 98 KPYFGARLS-----LNRASAHLGSDSFSKTSAGLGLVAGVAVTPN----- 140
DB 123 RPYTAGVNYTTFFDEKFNDTGKEAGLSDSLKDSWGMAGQVGLDYILNRDMLINASVWY 182
QY 141 VDLDAGYRYNVGK---VNTVKVRSGLSAGV 171
DB 183 MDIDTVRFKAGGQGOOSINTRLDPWVWFMSAGYR 216

RESULT 14
US-09-252-691C-9162

;; Sequence 9162, Application US/09252691C
;; GENERAL INFORMATION:
;; APPLICANT: Keith G. Weinstein et al.
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
;; FILE REFERENCE: 107196.135
;; CURRENT APPLICATION NUMBER: US/09/252,691C
;; CURRENT FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,145
;; PRIOR FILING DATE: 1998-07-24
;; PRIOR APPLICATION NUMBER: US 60/074,787
;; PRIOR FILING DATE: 1998-02-18
;; NUMBER OF SEQ ID NOS: 11326
;; SEQ ID NO 9162
;; LENGTH: 217
;; TYPE: PRT

;; ORGANISM: Enterobacter cloacae
US-09-252-691C-9162

Query Match 12.3%; Score 107; DB 16; Length 217;
Best Local Similarity 22.9%; Pred. No. 0.0037;
Matches 49; Conservative 38; Mismatches 79; Indels 48; Gaps 9;

QY 1 MKK-ALMALIALPAAALAEAGSGFYVQADAAHAKASSISGAKGSPRISAGYRI-ND 58
DB 8 MKLIAVAALLISLSGCAVYAHGAEFFIRAGSAIVRTESDNLGM-----GCFVNSNN 62
QY 59 LRFAYDT-----RYKNKAPSTDV-KLYISGASVY---YDFDTQSPV 97
DB 63 TOLGTFYMATDNGVELLAATPFRRHVGLGPTGDIATVHLPPIIMAOYFGDSSSKV 122
QY 98 KPYFGARLS-----LNRASAHLGSDSFSKTSAGLGLVAGVAVTPN----- 140
DB 123 RPYTAGVNYTTFFDEKFNDTGKEAGLSDSLKDSWGMAGQVGLDYILNRDMLINASVWY 182
QY 141 VDLDAGYRYNVGK---VNTVKVRSGLSAGV 171
DB 183 MDIDTVRFKAGGQGOOSINTRLDPWVWFMSAGYR 216

RESULT 15
US-08-065-442-2

;; Sequence 2, Application US/08065442
;; GENERAL INFORMATION:
;; APPLICANT: Kolattukudy, P. E.
;; TITLE OF INVENTION: Otitis Media Vaccine
;; NUMBER OF SEQUENCES: 2
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Calfee, Halter and Griswold
;; STREET: Suite 1800 800 Superior Avenue
;; CITY: Cleveland
;; STATE: Ohio
;; COUNTRY: U.S.A.
;; ZIP: 44114-2688
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentln Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/065,442
;; FILING DATE: 19930518
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Goltick, Mary E.
;; REGISTRATION NUMBER: 34,829
;; REFERENCE/DOCKET NUMBER: 22727/00102
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (216) 622-8458
;; TELEFAX: (216) 241-0816
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 359 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-065-442-2

Query Match 12.0%; Score 104; DB 4; Length 359;
Best Local Similarity 24.7%; Pred. No. 0.017;
Matches 56; Conservative 29; Mismatches 82; Indels 60; Gaps 11;

QY 1 MKKALALIALPAAALAEAG---SGFYVQADAA---HKASSISGASGSPRISAG 53
DB 1 MKKTAIAIVVAGLAASVAAQAPQENTFYAGYKAGQGSFHHGGINNCAIKKGLSS--NYG 59
QY 54 YRINDRFAYDTRRYKNKAPSTDFKLYISGASVYDFDTQSPV---KP-----YFGAR 104
DB 60 YRKNFTTYGV---FGYQILNQD---NFGLAELGTDGFAKALREAGKPRAKHTNHGAY 113

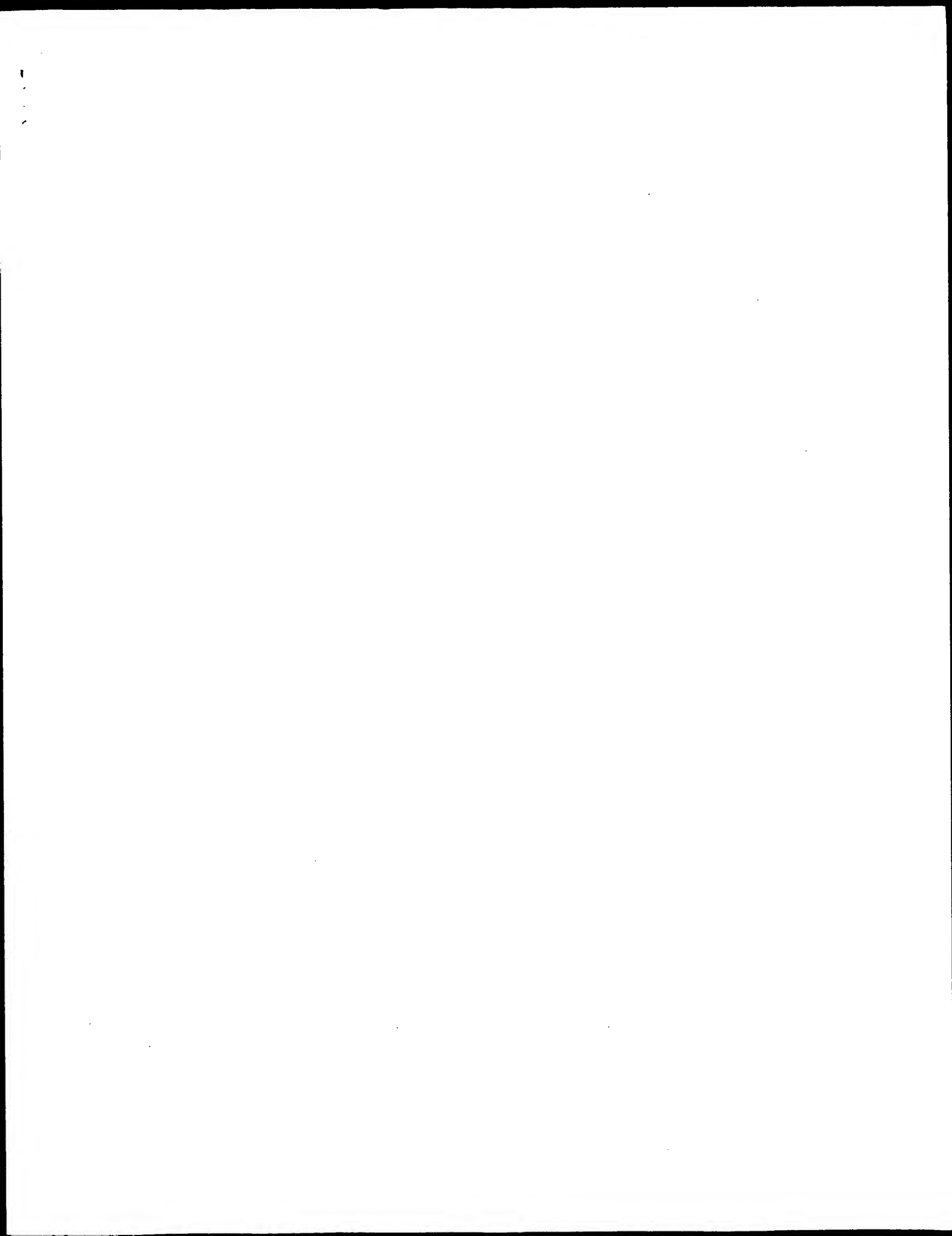
Tue Oct 29 09:23:23 2002

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[illegible]

Search completed: October 28, 2002, 16:11:24
Job time : 104.601 secs



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OM protein - protein search, using sw model

Run on: October 28, 2002, 16:01:19 ; Search time 35.6987 Seconds

(without alignments)
1465.185 Million cell updates/sec

Title: US-09-684-883-8

Perfect score: 870
Sequence: 1 MKKALALIALALPAALAE.....VNTKKNVSGELSGAVRK 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1112697 seqs, 300604653 residues

Total number of hits satisfying chosen parameters: 1112697

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_New:*

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13: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	870	100.0	174	US-09-684-883-8	Sequence 8, Appli
2	834	95.9	174	US-09-684-883-6	Sequence 6, Appli
3	825	94.8	174	US-09-684-883-2	Sequence 2, Appli
4	823.5	94.7	175	US-09-684-883-30	Sequence 30, Appli
5	813.5	93.5	175	US-09-684-883-4	Sequence 4, Appli
6	133	15.3	25	US-09-684-883-26	Sequence 26, Appli
7	106	12.2	353	US-10-203-942-9	Sequence 9, Appli
8	95	10.9	369	US-09-545-199F-153	Sequence 153, App
9	92	10.6	364	US-09-545-199F-151	Sequence 151, App
10	90	10.3	500	US-09-990-004A-149	Sequence 149, App
11	90	10.3	500	US-10-219-220-149	Sequence 149, App
12	87.5	10.1	576	US-09-791-537-117254	Sequence 117254,
13	87	10.0	16	US-09-684-883-15	Sequence 15, Appli
14	87	10.0	213	US-09-791-537-112202	Sequence 112202,
15	85	9.8	250	US-09-540-209B-9349	Sequence 9349, Ap
16	84.5	9.7	199	US-10-053-853A-8	Sequence 8, Appli
17	84.5	9.7	199	US-10-053-853A-80	Sequence 80, Appli
18	84.5	9.7	199	US-10-053-853A-760	Sequence 760, App
19	83.5	9.6	339	US-09-513-996A-67258	Sequence 67258, A
20	83.5	9.6	534	US-09-513-996A-7956	Sequence 7956, Ap

21	83	9.5	431	9	US-09-540-209B-7041	Sequence 7041, Ap
22	82.5	9.5	423	9	US-09-791-537-129337	Sequence 129337,
23	82.5	9.5	1082	13	US-60-360-039-17890	Sequence 17890, A
24	81.5	9.4	199	11	US-10-053-853A-970	Sequence 970, App
25	81	9.3	165	9	US-09-540-209B-7537	Sequence 7537, App
26	81	9.3	187	11	US-10-219-999-45753	Sequence 45753, A
27	81	9.3	229	11	US-10-219-999-59699	Sequence 59699, A
28	80	9.2	15	9	US-09-684-883-23	Sequence 23, Appli
29	80	9.2	163	9	US-09-791-537-98389	Sequence 98389, A
30	80	9.2	259	9	US-09-513-996A-57141	Sequence 57141, A
31	80	9.2	274	9	US-09-513-996A-57139	Sequence 57139, A
32	80	9.2	383	9	US-09-513-996A-45591	Sequence 45591, A
33	80	9.2	490	9	US-09-513-996A-45590	Sequence 45590, A
34	80	9.2	539	9	US-09-513-996A-45589	Sequence 45589, A
35	79	9.1	264	9	US-09-956-508A-4	Sequence 4, Appli
36	79	9.1	273	9	US-09-882-227-80	Sequence 80, Appli
37	79	9.1	400	9	US-09-513-996A-19382	Sequence 19382, A
38	79	9.1	507	9	US-09-513-996A-19381	Sequence 19381, A
39	79	9.1	551	13	US-60-360-039-15697	Sequence 15697, A
40	79	9.1	551	13	US-60-360-039-16088	Sequence 16088, A
41	79	9.1	556	9	US-09-513-996A-19380	Sequence 19380, A
42	79	9.1	624	13	US-60-360-039-15330	Sequence 15330, A
43	79	9.1	896	11	US-10-210-296-5	Sequence 5, Appli
44	78.5	9.0	199	11	US-10-053-853A-388	Sequence 388, App
45	78	9.0	15	9	US-09-684-883-14	Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-09-684-883-8
Sequence 8, Application US/09684883
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Hamel, Josee
Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,766
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8
US-09-684-883-8

Query Match 100.0%; Score 870; DB 9; Length 174;
Best Local Similarity 100.0%; Pred. No. 1,6e-81;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRKKNKAPSTDEKLYSIGASYIYDPDQSPVKPYFGARLSLNRASVHLGSSDSF 120
DB 61 FAVDYTRKKNKAPSTDEKLYSIGASYIYDPDQSPVKPYFGARLSLNRASVHLGSSDSF 120
QY 121 SKTSAGLVLAGVSAVTPNVLDAGYRNYVGKVTYKVRSGELSGAYRVKF 174
DB 121 SKTSAGLVLAGVSAVTPNVLDAGYRNYVGKVTYKVRSGELSGAYRVKF 174

RESULT 2
US-09-684-883-6
Sequence 6, Application US/09684883

GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/684,883
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-684-883-6

Query Match 95.9%; Score 834; DB 9; Length 174;
Best Local Similarity 95.4%; Pred. No. 8.1e-78;
Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRKKNKAPSTDEKLYSIGASYIYDPDQSPVKPYFGARLSLNRASVHLGSSDSF 120
DB 61 FAVDYTRKKNKAPSTDEKLYSIGASYIYDPDQSPVKPYFGARLSLNRASVHLGSSDSF 120
QY 121 SKTSAGLVLAGVSAVTPNVLDAGYRNYVGKVTYKVRSGELSGAYRVKF 174
DB 121 SKTSAGLVLAGVSAVTPNVLDAGYRNYVGKVTYKVRSGELSGAYRVKF 174

RESULT 3
US-09-684-883-2
Sequence 2, Application US/09684883

GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/684,883
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-684-883-2

Query Match 94.8%; Score 825; DB 9; Length 174;
Best Local Similarity 94.3%; Pred. No. 6.9e-77;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60

DB 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASVYDFDTQSPVKPYFGARLSLNRAASHLGGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASVYDFDTQSPVKPYFGARLSLNRAASHLGGSDSF 120
QY 121 SKTSAGLGVLAGSVYAVTPNVDDAGRYRNYGKVTYVKNVSGELSGAGYRVKF 174
DB 121 SQSTSGLGVLAGSVYAVTPNVDDAGRYRNYGKVTYVKNVSGELSGAGYRVKF 174

RESULT 4
US-09-684-883-30
Sequence 30, Application US/09684883
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Hamel, Denise
Martin, Denis
Rioux, Clement
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: linear
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-684-883-30

Query Match 94.7%; Score 823.5; DB 9; Length 175;
Best Local Similarity 94.9%; Pred. No. 9.9e-77;
Matches 166; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASVYDFDTQSPVKPYFGARLSLNRAASHLGGSDS 119

DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASVYDFDTQSPVKPYFGARLSLNRAASHLGGSDS 120
QY 120 FSKTSAGLGVLAGSVYAVTPNVDDAGRYRNYGKVTYVKNVSGELSGAGYRVKF 174
DB 121 SQSTSGLGVLAGSVYAVTPNVDDAGRYRNYGKVTYVKNVSGELSGAGYRVKF 175

RESULT 5
US-09-684-883-4
Sequence 4, Application US/09684883
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Hamel, Denise
Martin, Denis
Rioux, Clement
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-684-883-4

Query Match 93.5%; Score 813.5; DB 9; Length 175;
Best Local Similarity 93.7%; Pred. No. 1.1e-75;
Matches 164; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASVYDFDTQSPVKPYFGARLSLNRAASHLGGSDS 119
DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASVYDFDTQSPVKPYFGARLSLNRAASHLGGSDS 120
QY 120 FSKTSAGLGVLAGSVYAVTPNVDDAGRYRNYGKVTYVKNVSGELSGAGYRVKF 174
DB 121 SQSTSGLGVLAGSVYAVTPNVDDAGRYRNYGKVTYVKNVSGELSGAGYRVKF 175

[illegible]

Db 119 PSEVLPDLDDYGVKAVGIAVVRANDKKY-GAE-NINEST-----KHKHLKASTIIIGAGV 170

Db 134 SYAVTPNVDLDAGRYRNYGVKNTVKN--VRSG-----ELSGAVRKFF 174

Db 171 EYALTP--ELAAAREYQLNAGLAKALVRSQTQDVFQYAPDISHSVTNGSLRFF 224

Query Match 10.1%; Score 87.5; DB 9; Length 576;
 Best Local Similarity 25.1%; Pred. No. 2.8;
 Matches 43; Conservative 28; Mismatches 59; Indels 41; Gaps 9;

OY 19 AEGASGEYVQDA-----AHAKASSIGS-AKGFSPRISA-GYRINDLRPAVDYRK 67
 DB 432 ASADTKRPAATDALTCKGNALTKNAKSTITDLGTVDGDFDGRVTLALDTKNAL----- 483

OY 68 YKNYKASTDEKLYSIGASYIDPDTSPPV---KPYFGARLSINRAHILGSGDSFSRKT 123
 DB 484 --DKRVNAFDRIALDSKVENGAQAALSLGLFQPSYCKFN---ATAALGGYGSASAV 538

OY 124 SAGIGVLAGSYAVTPNVDLDAGTRINIVGRVNTVKNVSGELSGAYRVKPF 174
 DB 539 AIGAG-----YRVNPMIAFKAG-----AALNTSGN-KKGSYNIQVNYEEF 576

RESULT 13
 US-09-684-883-15
 ; Sequence 15, Application US/09684883
 ; GENERAL INFORMATION:
 ; APPLICANT: Brodeur, Bernard R
 ; Hamel, Josee
 ; Rioux, Clement
 ; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/684,883
 ; FILING DATE: 06-Oct-2000
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/913,362
 ; FILING DATE: 13-NOV-1997
 ; APPLICATION NUMBER: US 08/406,362
 ; FILING DATE: 17-MAR-1995
 ; APPLICATION NUMBER: US 60/001,983
 ; FILING DATE: 04-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bent, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 047998/0128
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: Neisseria meningitidis
 ; STRAIN: 608B
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 ; US-09-684-883-15

Query Match 10.0%; Score 87; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61 FAVDYTRYKNYKAPST 76
 DB 1 FAVDYTRYKNYKAPST 16

RESULT 14
 US-09-791-537-112202
 ; Sequence 112202, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Biomolix, Inc.
 ; APPLICANT: Dede, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 112202
 ; LENGTH: 213
 ; TYPE: PRT
 ; ORGANISM: Brucella canis
 ; US-09-791-537-112202

Query Match 10.0%; Score 87; DB 9; Length 213;
 Best Local Similarity 26.1%; Pred. No. 0.87;
 Matches 48; Conservative 30; Mismatches 72; Indels 34; Gaps 9;

OY 14 PAAALAEASGEYVQDAHAHAKASSLSGAKGFSPRISA---GYRINDLRPAVDYTRYK 69
 DB 41 PYSWAGGYTGLYLTGYGNKAK-TSTVGSIKPDMDKAGAFAGWNFQKDIYGVGEGDAGY 99

OY 70 NYKAPSTD-----FKLYSIGASYIDPDTSPPVYKPF-----GARSLNRAHILGGS 117
 DB 100 SWAKSKDGLVYKQGF-GLSLRAVGYDL--NPWAPYLTGIAISOITKL-----NGL 149

OY 118 DESFKTSAGIGVLAGSYAVTPNVDLDAGYRY-----NYGKVTYVN-VRSGLSAGV 170
 DB 150 DESKRFVGTAGAGLEKLTINILIGREYRYTOYSNNNYDLAGTYVANKLDJTDIRGI 209

OY 171 RYKF 174
 DB 210 GYKF 213

RESULT 15
 US-09-540-209B-9349
 ; Sequence 9349, Application US/09540209B
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES
 ; FILE REFERENCE: 2709,1001-001
 ; CURRENT APPLICATION NUMBER: US/09/540,209B
 ; CURRENT FILING DATE: 2000-04-04
 ; NUMBER OF SEQ ID NOS: 10444
 ; SEQ ID NO 9349
 ; LENGTH: 250
 ; TYPE: PRT
 ; ORGANISM: B. fragilis
 ; US-09-540-209B-9349

Query Match 9.8%; Score 85; DB 9; Length 250;
 Best Local Similarity 27.3%; Pred. No. 1.7;
 Matches 44; Conservative 20; Mismatches 57; Indels 40; Gaps 9;

OY 1 MKK-ALMALIALPAA-----ALAEASG---FYVQA-----DAHAKASSS 39
 DB 32 MKKVTLVALLALSSCNSDPKFNKGVSGADGKMLYLEASGLEGIYPLDSILKKGGS 91
 OY 40 LGSAGFSRISAGYRI-----NDLRPAVDYTRYKNYKAPSTDFK-LYSIGASYIDPDQ 94

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Db 92 F-SFKOLRPESEPFYRLVREDKYNFSVDSTETVSIQAPYTDSTATVEGS-----ENS 145
QY 95 SPVKPYFGARLSINR-----ASAHLGSDSFSKTSAGL 127
Db 146 AKIKELTIKQVRLQKVDALVKAAQAHQLGNDVFEDSLAVL 186

Search completed: October 28, 2002, 16:13:53
Job time : 36.6987 secs

